



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 143151

TO: Ruixiang Li
Location: rem/4d75/4c70
Art Unit: 1646
Friday, February 11, 2005

Case Serial Number: 09/927267

From: Mary Jane Ruhl
Location: Biotech-Chem Library
Remsen 1-A-62
Phone: 571-272-2524

maryjane.ruhl@uspto.gov

Search Notes

Examiner Li,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl
Technical Information Specialist
STIC
Remsen 1-A-62
Ext. 22524

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From: Li, Ruixiang
Sent: Tuesday, January 25, 2005 10:44 AM
To: STIC-Biotech/ChemLib
Subject: Sequence search of Application No.09/927,267

Please do a standard search on:

- (i). SEQ ID NOS: 1, 2, and 3 against interference nucleic acid databases;
- (ii). SEQ ID NO: 1 against interference amino acid databases.

Thank you very much!

Ruixiang Li
GAU 1646
REM 4D75
Mail Box 4C70
(571) 272-0875

RECEIVED
JAN 25 2005
STIC

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA Sequence: # _____
AA Sequence: # _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIS: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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OM protein - protein search, using sw model

Run on: February 10, 2005, 03:39:26 ; Search time 85 Seconds

(without alignments)
2444.016 Million cell updates/sec

Title: US-09-927-267-1

Perfect score: 2989
Sequence: 1 MSQDTRKVTSSPPAPSKA.....EGTSKDEGRASQGEPPPE 575

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Published Applications AA:*

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20: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2989	100.0	575	US-09-735-932-2	Sequence 2, Appl1
2	2989	100.0	575	US-09-927-267-1	Sequence 2, Appl1
3	2989	100.0	575	US-10-207-951-2	Sequence 2, Appl1
4	2984	99.8	575	US-09-842-758-30	Sequence 30, Appl1
5	2984	99.8	575	US-10-174-333-30	Sequence 30, Appl1
6	2984	99.8	575	US-10-311-624-1	Sequence 1, Appl1
7	2957.5	98.9	578	US-09-842-758-28	Sequence 28, Appl1
8	2957.5	98.9	578	US-10-174-333-28	Sequence 28, Appl1
9	2811	94.0	575	US-09-735-932-4	Sequence 4, Appl1
10	2811	94.0	575	US-09-927-267-16	Sequence 16, Appl1
11	2811	94.0	575	US-09-842-758-74	Sequence 74, Appl1
12	2811	94.0	575	US-10-174-333-74	Sequence 74, Appl1
13	2394	80.1	1704	US-10-207-951-4	Sequence 4, Appl1

14	1568	52.5	663	14	US-10-029-677-16	Sequence 16, Appl1
15	1565	52.4	664	14	US-10-295-573-5	Sequence 5, Appl1
16	1562	52.3	664	9	US-09-735-927-4	Sequence 4, Appl1
17	1562	52.3	732	10	US-09-842-758-73	Sequence 73, Appl1
18	1562	52.3	732	10	US-10-029-677-15	Sequence 15, Appl1
19	1562	52.3	732	15	US-10-174-333-73	Sequence 73, Appl1
20	1558	52.1	664	14	US-10-029-677-18	Sequence 18, Appl1
21	1558	52.1	664	14	US-10-087-217-2	Sequence 2, Appl1
22	1558	52.1	664	14	US-10-295-573-8	Sequence 8, Appl1
23	1554	52.0	634	14	US-10-295-573-7	Sequence 7, Appl1
24	1554	52.0	664	14	US-10-087-217-6	Sequence 6, Appl1
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26	1549.5	51.8	694	10	US-09-842-758-75	Sequence 75, Appl1
27	1549.5	51.8	694	14	US-09-855-828-14	Sequence 14, Appl1
28	1549.5	51.8	694	11	US-10-345-680-26	Sequence 26, Appl1
29	1549.5	51.8	694	15	US-10-174-333-75	Sequence 75, Appl1
30	1549	51.8	664	14	US-10-087-217-4	Sequence 4, Appl1
31	1547	51.8	664	14	US-10-029-677-17	Sequence 17, Appl1
32	1545	51.7	664	14	US-10-087-217-8	Sequence 8, Appl1
33	1538.5	51.5	690	11	US-09-855-828-15	Sequence 15, Appl1
34	1535	51.4	664	9	US-09-735-927-2	Sequence 2, Appl1
35	1535	51.4	664	13	US-10-034-843-2	Sequence 2, Appl1
36	1535	51.4	664	14	US-10-168-651-7	Sequence 7, Appl1
37	1535	51.4	664	14	US-10-114-153-18	Sequence 18, Appl1
38	1532	51.3	664	14	US-10-029-677-24	Sequence 24, Appl1
39	1529	51.2	664	14	US-10-029-677-2	Sequence 2, Appl1
40	1208	40.4	239	14	US-10-189-507-10	Sequence 10, Appl1
41	1196	40.0	239	14	US-10-189-507-6	Sequence 6, Appl1
42	779	26.1	239	14	US-10-189-507-5	Sequence 5, Appl1
43	773	25.9	239	14	US-10-189-507-9	Sequence 9, Appl1
44	769	25.7	239	14	US-10-189-507-12	Sequence 12, Appl1
45	655	21.9	809	11	US-09-855-828-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-09-735-932-2
Sequence 2, Application US/09735932
Patent No. US20020037546A1
GENERAL INFORMATION:
APPLICANT: GUEGLER, Karl et al
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUM AN TRANSPORTER PROTEINS,
FILE REFERENCE: CL000663
CURRENT APPLICATION NUMBER: US/09/735,932
CURRENT FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 575
TYPE: PRT
ORGANISM: Human
US-09-735-932-2

Query Match 100.0%, Score 2989, DB 9, Length 575;
Best Local Similarity 100.0%, Pred. No. 1.7e-253;
Matches 575; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	1	MSQDTRKVTSSPPAPSKARLLPVLDPSGGYYTMMINTWEPVWYNLIIVCRACFPD	60
QY	61	LDHGYLVAMLVLDYTSDDLVDMMVFRHTGFLBEGGILVVDKGRISRRVRTWSEFLDIA	120
DB	61	LDHGYLVAMLVLDYTSDDLVDMMVFRHTGFLBEGGILVVDKGRISRRVRTWSEFLDIA	120
QY	121	SIMPTDYYVVRIGPHTPTLRNFRAPRLFEAFPRTERTRTYNPAFRAKMLTYFVVI	180
DB	121	SIMPTDYYVVRIGPHTPTLRNFRAPRLFEAFPRTERTRTYNPAFRAKMLTYFVVI	180

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Db 181 HNSCLYFALSRYLGFGRDAWVYPPAOPGFERLRQYLYSFYSTLLITLVGDTPEPPAR 240
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Db 241 EEEYLFPMVGDFFLLAVMGFATIMGSMSSVLYNNMTADAAFPYDHALYKCYMKLOHVNARKLE 300
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Db 301 RRVIDMYOHLQINKKMTNEVALIQLHLPRLRAEVAVSHLSTLSRVQIFONCEASLLEEL 360
QY 361 VLKLOPQYTSPEGYVCRKGDIGQEMYIIREGQLAVVADGITOYAVLAGLYFGEISITIN 420
Db 361 VLKLOPQYTSPEGYVCRKGDIGQEMYIIREGQLAVVADGITOYAVLAGLYFGEISITIN 420
QY 421 IKGNMGNRRRTANIKSLGYSDLPCLSKEDLREVLSEYPOAQTIMEKREILLKNNKLDV 480
Db 421 IKGNMGNRRRTANIKSLGYSDLPCLSKEDLREVLSEYPOAQTIMEKREILLKNNKLDV 480
QY 481 NAEAAEIALQEAATESRLRGIDQDLQTKFARLLAELESSALKIAYRIERLEMOTREMP 540
Db 481 NAEAAEIALQEAATESRLRGIDQDLQTKFARLLAELESSALKIAYRIERLEMOTREMP 540
QY 541 MPEDLAADDEGPEBEGTSKDEGRASQEGPPGPE 575
Db 541 MPEDLAADDEGPEBEGTSKDEGRASQEGPPGPE 575
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RESULT 2
US-09-927-267-1

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/ Sequence 1, Application US/09927267
/ Publication No. US20020182691A1
/ GENERAL INFORMATION:
/ APPLICANT: Crech, Christopher D.
/ APPLICANT: Jegla, Timothy J.
/ APPLICANT: ICagen, Inc.
/ TITLE OF INVENTION: CNG2B. A No. US20020182691A1 Human Cyclic Nucleotide-Gated Ion
/ TITLE OF INVENTION: Channel
/ FILE REFERENCE: 018512-006510US
/ CURRENT APPLICATION NUMBER: US/09/927,267
/ CURRENT FILING DATE: 2001-08-10
/ PRIOR APPLICATION NUMBER: US 60/226,253
/ PRIOR FILING DATE: 2000-08-17
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 1
/ LENGTH: 575
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: cyclic nucleotide-gated cation channel 2B (CNG2B)
US-09-927-267-1
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Query Match 100.0%; Score 2989; DB 9; Length 575;
Best Local Similarity 100.0%; Pred. No. 1.7e-253;
Matches 575; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 LOHGIVLAVMLVLDYSDLLYLIDMNVRFHTGFLFEGGILVVDKRISSRYRTWSFFLDLA 120
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Db 121 SLMPDVVVYRLGPHPTLRINRFLAPRLFEAFDRTEFTRAYNAPFIADLMYIFVVI 180
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Db 181 HNSCLYFALSRYLGFGRDAWVYPPAOPGFERLRQYLYSFYSTLLITLVGDTPEPPAR 240
QY 241 EEEYLFPMVGDFFLLAVMGFATIMGSMSSVLYNNMTADAAFPYDHALYKCYMKLOHVNARKLE 300
Db 241 EEEYLFPMVGDFFLLAVMGFATIMGSMSSVLYNNMTADAAFPYDHALYKCYMKLOHVNARKLE 300
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RESULT 3
US-10-207-951-2

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/ Sequence 2, Application US/10207951
/ Publication No. US20030013156A1
/ GENERAL INFORMATION:
/ APPLICANT: Karl GUEGLER et al.
/ TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
/ TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS
/ TITLE OF INVENTION: AND USUS THEREOF
/ FILE REFERENCE: CL000663CON
/ CURRENT APPLICATION NUMBER: US/10/207,951
/ CURRENT FILING DATE: 2002-07-31
/ PRIOR APPLICATION NUMBER: 09/735,932
/ PRIOR FILING DATE: 2000-12-14
/ PRIOR APPLICATION NUMBER: 60/211,223
/ PRIOR FILING DATE: 2000-06-13
/ NUMBER OF SEQ ID NOS: 25
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 575
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-207-951-2
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Query Match 100.0%; Score 2989; DB 14; Length 575;
Best Local Similarity 100.0%; Pred. No. 1.7e-253;
Matches 575; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 LOHGIVLAVMLVLDYSDLLYLIDMNVRFHTGFLFEGGILVVDKRISSRYRTWSFFLDLA 120
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Db 121 SLMPDVVVYRLGPHPTLRINRFLAPRLFEAFDRTEFTRAYNAPFIADLMYIFVVI 180
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Db 181 HNSCLYFALSRYLGFGRDAWVYPPAOPGFERLRQYLYSFYSTLLITLVGDTPEPPAR 240
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DB 361 VKLQPOPTYSPEEYCRKGDIGQEWYIIREGOLAVVADGITQYAVLAGLYFGEISITIN 420
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RESULT 4

US-09-842-758-30
Sequence 30, Application US/09842758
Publication No. US20030083244A1
GENERAL INFORMATION:
APPLICANT: Vernet, Corine A. M.
APPLICANT: Fernandes, Elma R.
APPLICANT: Gerlach, Valerie
APPLICANT: Shinkens, Richard A.
APPLICANT: Malvankar, Uriel M.
APPLICANT: Boldog, Ferenc L.
APPLICANT: Zernusen, Bryan D.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Majumder, Kumud
APPLICANT: Tchernev, Velizar T.
APPLICANT: Padigaru, Muralidhara
APPLICANT: Patturajan, Meera
APPLICANT: Burgess, Catherine E.
APPLICANT: Gangoli, Bsha A.
APPLICANT: Smithson, Glenda
APPLICANT: Raestelli, Luca
APPLICANT: MacDougall, John R.
APPLICANT: Taupier, Raymond J.
APPLICANT: Groese, William M.
APPLICANT: Edward, Szekeres S.
TITLE OF INVENTION: No. US20030083244A1e1 Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 15966-783
CURRENT APPLICATION NUMBER: US/09/842,758
CURRENT FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: 60/200,158
PRIOR FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: 60/200,613
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,780
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/201,006
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,007
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,236
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,238
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,186
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 60/201,474
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 60/201,508
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 60/220,591

PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: 60/232,678
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 60/263,217
PRIOR FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: 60/265,160
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 113
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO: 30
LENGTH: 575
TYPE: PRT
ORGANISM: Homo sapiens
US-09-842-758-30

Query Match 99.8%; Score 2984; DB 10; Length 575;
Best Local Similarity 99.8%; Pred. No. 4,8e-253; Indels 0; Gaps 0;
Matches 574; Conservative 0; Mismatches 1;

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DB 1 MSQDTKVKTTSSPPAPSKARKLPLVDPSSGDYYMMINTWVFPVMNLIILVCRACFPD 60
QY 61 LQHGVLVAMVLVDYTSLLIYLLDMVVRPHGFLQGLIYVDKRISSRYVRTWSPFLDLA 120
DB 61 LQHGVLVAMVLVDYTSLLIYLLDMVVRPHGFLQGLIYVDKRISSRYVRTWSPFLDLA 120
QY 121 SLMPDVTYVYVRLGHTPTPLRLNRLRFLRAPRLPEAFPRTRTAYPAFRIAKMLYIPVYI 180
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DB 181 HNSCLYFALSRYLGFGRDAMWYPPDAPGFERLRQYLYSFYSTLLITTVGDTPPPAR 240
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DB 241 EEEYLFMYGDFLLAVMGFATIMGSSSVIYNNMTADAAPYPDHALVKKYMKLOHYNRKLE 300
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DB 301 RVIDWYQHLOINKMTNEVALLOHLPERLRAEVAVSHLSTLSRVQIFONCEASLLEEL 360
QY 361 VKLQPOPTYSPEEYCRKGDIGQEWYIIREGOLAVVADGITQYAVLAGLYFGEISITIN 420
DB 361 VKLQPOPTYSPEEYCRKGDIGQEWYIIREGOLAVVADGITQYAVLAGLYFGEISITIN 420
QY 421 IKGNNSGNRRNTANIKSLGSDLFCLSKEDLREVLSEYPOAQITMEKREIILKNKLDV 480
DB 421 IKGNNSGNRRNTANIKSLGSDLFCLSKEDLREVLSEYPOAQITMEKREIILKNKLDV 480
QY 481 NAEAEIALQEAATESRLRGDLODDLOTKPARLLAELESSALKIAYRIERLEWOTREMP 540
DB 481 NAEAEIALQEAATESRLRGDLODDLOTKPARLLAELESSALKIAYRIERLEWOTREMP 540
QY 541 MPEDLAADDEGEPEEGTSKDEEGRASQEGPPGPE 575
DB 541 MPEDLAADDEGEPEEGTSKDEEGRASQEGPPGPE 575

RESULT 5

US-10-174-333-30
Sequence 30, Application US/10174333
Publication No. US20040029220A1
GENERAL INFORMATION:
APPLICANT: Vernet, Corine A. M.
APPLICANT: Fernandes, Elma R.
APPLICANT: Gerlach, Valerie
APPLICANT: Malvankar, Uriel M.
APPLICANT: Boldog, Ferenc L.
APPLICANT: Zernusen, Bryan D.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Majumder, Kumud

```

; APPLICANT: Tchernov, Velizar T.
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Paturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Gangoli, Baha A.
; APPLICANT: Smithson, Glenda
; APPLICANT: Rastelli, Luca
; APPLICANT: MacDougall, John R.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Grose, William M.
; APPLICANT: Szekeres, Edward S.
; APPLICANT: Alsobrook, John P.
; APPLICANT: Anderson, David M.
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Li, Li
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-783 CIP1
; CURRENT APPLICATION NUMBER: US/10/174,333
; PRIOR FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 60/193,664
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/194,614
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 60/195,063
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,066
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,067
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,068
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,069
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,070
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,510
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/219,855
; PRIOR FILING DATE: 2000-07-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: Cytosql version 0.1
; SEQ ID NO 30
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-174-333-30

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Query Match          99.8%; Score 2984; DB 15; Length 575;
Best Local Similarity 99.8%; Pred. No. 4.8e-253;
Matches 574; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSODTKVKTSSPPAPSKARKLLPVLDPSGDYYWMLNTMVPVWNLILVCRACFPD 60
DB 1 MSODTKVKTSSPPAPSKARKLLPVLDPSGDYYWMLNTMVPVWNLILVCRACFPD 60
QY 61 LQHGVLVAMLVLDYTSDDLTYLLDMVVRFTGFEQGLIVDKRISRVRYSFPLDLA 120
DB 61 LQHGVLVAMLVLDYTSDDLTYLLDMVVRFTGFEQGLIVDKRISRVRYSFPLDLA 120
QY 121 SLMPDVVVYVRLGPHPTLRNLRLAPRLFEAFDRTETRTAYVNAFRIAKMLYIFVVI 180
DB 121 SLMPDVVVYVRLGPHPTLRNLRLAPRLFEAFDRTETRTAYVNAFRIAKMLYIFVVI 180
QY 181 HNMSCIFYALSRYLGFGRDAMVYDPDPAQGFERLRQYLYSFYSTLILTTVGDPDPPAR 240
DB 181 HNMSCIFYALSRYLGFGRDAMVYDPDPAQGFERLRQYLYSFYSTLILTTVGDPDPPAR 240
QY 241 EEEYLFVAGDFLLAVNGFATIMGSMSSVYNNMTADAFAYPDHALVKKYMKLOHVRKLE 300
DB 241 EEEYLFVAGDFLLAVNGFATIMGSMSSVYNNMTADAFAYPDHALVKKYMKLOHVRKLE 300

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QY 301 RRVIDMYQHLOINKKMTNEVALLOHLPERLRABVAVSHLSTLSRVQIFONCEASLLEBL 360
DB 301 RRVIDMYQHLOINKKMTNEVALLOHLPERLRABVAVSHLSTLSRVQIFONCEASLLEBL 360
QY 361 VLKLOPQYTSPEEYVCRKGDIGQEWYIIRREGOLAVADADGTQYVAVLGAAGYFGEISITIN 420
DB 361 VLKLOPQYTSPEEYVCRKGDIGQEWYIIRREGOLAVADADGTQYVAVLGAAGYFGEISITIN 420
QY 421 IKGNMGNRRRTANISLGSYDLFCLSKEDLRBVSEYPOAQTMEKREILLKXNKLDV 480
DB 421 IKGNMGNRRRTANISLGSYDLFCLSKEDLRBVSEYPOAQTMEKREILLKXNKLDV 480
QY 481 NAAEALAOEATSRRLRGLOQDLDLQTKFARILAEISSALKTAYRLEELWOTRMP 540
DB 481 NAAEALAOEATSRRLRGLOQDLDLQTKFARILAEISSALKTAYRLEELWOTRMP 540
QY 541 MPEDIAEADDEGEPEEGTSGKDEGRASQEGPGE 575
DB 541 MPEDIAEADDEGEPEEGTSGKDEGRASQEGPGE 575

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RESULT 6
US-10-311-624-1
; Sequence 1, Application US/10311624
; Publication No. US20040127683A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: RAUMANN, Brigitte E.
; APPLICANT: Sanjwal, Madhu S.
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: Walla, Narinder K.
; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
; FILE REFERENCE: SI-0141 ECT
; CURRENT APPLICATION NUMBER: US/10/311,624
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: 60/215,391
; PRIOR FILING DATE: 2000-06-29
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 6703242CD1
US-10-311-624-1

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Query Match          99.8%; Score 2984; DB 16; Length 575;
Best Local Similarity 99.8%; Pred. No. 4.8e-253;
Matches 574; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSODTKVKTSSPPAPSKARKLLPVLDPSGDYYWMLNTMVPVWNLILVCRACFPD 60
DB 1 MSODTKVKTSSPPAPSKARKLLPVLDPSGDYYWMLNTMVPVWNLILVCRACFPD 60
QY 61 LQHGVLVAMLVLDYTSDDLTYLLDMVVRFTGFEQGLIVDKRISRVRYSFPLDLA 120
DB 61 LQHGVLVAMLVLDYTSDDLTYLLDMVVRFTGFEQGLIVDKRISRVRYSFPLDLA 120
QY 121 SLMPDVVVYVRLGPHPTLRNLRLAPRLFEAFDRTETRTAYVNAFRIAKMLYIFVVI 180
DB 121 SLMPDVVVYVRLGPHPTLRNLRLAPRLFEAFDRTETRTAYVNAFRIAKMLYIFVVI 180
QY 181 HNMSCIFYALSRYLGFGRDAMVYDPDPAQGFERLRQYLYSFYSTLILTTVGDPDPPAR 240
DB 181 HNMSCIFYALSRYLGFGRDAMVYDPDPAQGFERLRQYLYSFYSTLILTTVGDPDPPAR 240
QY 241 EEEYLFVAGDFLLAVNGFATIMGSMSSVYNNMTADAFAYPDHALVKKYMKLOHVRKLE 300
DB 241 EEEYLFVAGDFLLAVNGFATIMGSMSSVYNNMTADAFAYPDHALVKKYMKLOHVRKLE 300
QY 301 RRVIDMYQHLOINKKMTNEVALLOHLPERLRABVAVSHLSTLSRVQIFONCEASLLEBL 360

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Db 301 RRVIMWQHLQINKKMTNEVALIQLPELRRAEVAVSVHLSTLSRVQIFQNCESASLEEL 360
Qy 361 VKLKLPQYTSPEGYVCRKGDIGQEMYYIRREGOLAVVADGITYAVLAGLYGGEISII 420
Db 361 VKLKLPQYTSPEGYVCRKGDIGQEMYYIRREGOLAVVADGITYAVLAGLYGGEISII 420
Qy 421 IKGNMGNRRNTANISLGYSDLPCLSKEDLRVLSYPOQTIIMEKREILLKXNKLDV 480
Db 421 IKGNMGNRRNTANISLGYSDLPCLSKEDLRVLSYPOQTIIMEKREILLKXNKLDV 480
Qy 481 NAEAEIALQEAATESRLRGDLDOQLDLQTKFARLLAELESSALKIAYRIERLEWQTRMP 540
Db 481 NAEAEIALQEAATESRLRGDLDOQLDLQTKFARLLAELESSALKIAYRIERLEWQTRMP 540
Qy 541 MPEDLAADDEGEPEBEGTSKDEEGRAHQGPPE 575
Db 541 MPEDLAADDEGEPEBEGTSKDEEGRAHQGPPE 575

RESULT 7

US-09-842-758-28
; Sequence 28, Application US/09842758
; Publication No. US20030083244A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A. M.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Zehusen, Bryan D.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Patcurajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Gangoli, Beha A.
; APPLICANT: Smithson, Glenda
; APPLICANT: MacDougall, John R.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Grose, William M.
; APPLICANT: Edward, Szekeres S.
; APPLICANT: Alsbrook II, John P.
; TITLE OF INVENTION: No. US20030083244A1e1 Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-783
; CURRENT APPLICATION NUMBER: US/09/842,758
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/200,158
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 60/200,613
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,780
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/201,006
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/201,007
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/201,236
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/201,238
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/201,186
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 60/201,474
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/201,508
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/220,591
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: 60/232,678

; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 60/263,217
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: 60/265,160
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 578
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-842-758-28

Query Match 98.9%; Score 2957.5; DB 10; Length 578;
Best Local Similarity 99.5%; Pred. No. 1e-250;
Matches 575; Conservative 0; Mismatches 0; Indels 3; Gaps 3;

Qy 1 MSQDTKVTSSPPAPSKA-RKLLPVLDPGSDYYWMLNTMVFVMTNLIIIVCRACFP 59
Db 1 MSQDTKVTSSPPAPSKARRKLLPVLDPGSDYYWMLNTMVFVMTNLIIIVCRACFP 60
Qy 60 DLQHGVLAVMLVDYTSLLVLDVVRFT-GLIEGILLVVDKGRISRYRTWSFFLD 118
Db 61 DLQHGVLAVMLVDYTSLLVLDVVRFTGGLFEGILLVVDKGRISRYRTWSFFLD 120
Qy 119 LASLMPDVVYVRLGPHPTLRNLNRLAPRLEAFDTERRTAYPNAFRIAKMLYIFV 178
Db 121 LASLMPDVVYVRLGPHPTLRNLNRLAPRLEAFDTERRTAYPNAFRIAKMLYIFV 180
Qy 179 VIHNSCLYFALSRYLFGDAMVYDPAQGFERLRQVLYSFYSTLIITVGDTPP 238
Db 181 VIHNSCLYFALSRYLFGDAMVYDPAQGFERLRQVLYSFYSTLIITVGDTPP 240
Qy 239 ARREYLPWNGDFLLAWGFAITGSMSSVLYNMNTAAPFDPBALVKKWKLVNRK 298
Db 241 ARREYLPWNGDFLLAWGFAITGSMSSVLYNMNTAAPFDPBALVKKWKLVNRK 300
Qy 299 LERRVIDWYQHLOINKKMTNEVALIQHLPERLRRAEVAVSVHLSTLSRVQIFQNCESASLE 358
Db 301 LERRVIDWYQHLOINKKMTNEVALIQHLPERLRRAEVAVSVHLSTLSRVQIFQNCESASLE 360
Qy 359 ELVNLQPYTSPEGYVCRKGDIGQEMYYIRREGOLAVVADGITYAVLAGLYGGEISI 418
Db 361 ELVNLQPYTSPEGYVCRKGDIGQEMYYIRREGOLAVVADGITYAVLAGLYGGEISI 420
Qy 419 INIKGNMGNRRNTANISLGYSDLPCLSKEDLRVLSYPOQTIIMEKREILLKXNK 477
Db 421 INIKGNMGNRRNTANISLGYSDLPCLSKEDLRVLSYPOQTIIMEKREILLKXNK 480
Qy 478 LDVNAEAEIALQEAATESRLRGDLDOQLDLQTKFARLLAELESSALKIAYRIERLEWQTR 537
Db 481 LDVNAEAEIALQEAATESRLRGDLDOQLDLQTKFARLLAELESSALKIAYRIERLEWQTR 540
Qy 538 EWPMPEDLAADDEGEPEBEGTSKDEEGRAHQGPPE 575
Db 541 EWPMPEDLAADDEGEPEBEGTSKDEEGRAHQGPPE 578

RESULT 8
US-10-174-333-28
; Sequence 28, Application US/10174333
; Publication No. US20040029220A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A. M.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Zehusen, Bryan D.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Padigar, Muralidhara

```

/ APPLICANT: Paturajan, Meera
/ APPLICANT: Burgess, Catherine E.
/ APPLICANT: Gangoli, Sana A.
/ APPLICANT: Smithson, Glenda
/ APPLICANT: Raetelli, Luca
/ APPLICANT: MacDougall, John R.
/ APPLICANT: Taupier, Raymond J.
/ APPLICANT: Grose, William M.
/ APPLICANT: Szekeres, Edward S.
/ APPLICANT: Alsobrook, John P.
/ APPLICANT: Anderson, David W.
/ APPLICANT: Guo, Xiaojia (Sasha)
/ APPLICANT: Li, Li
/ APPLICANT: Zhong, Mei
/ TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
/ FILE REFERENCE: 15966-783 CIP1
/ CURRENT FILING DATE: US/10/174,333
/ PRIOR FILING DATE: 2002-06-18
/ PRIOR APPLICATION NUMBER: 60/193,664
/ PRIOR FILING DATE: 2000-03-31
/ PRIOR APPLICATION NUMBER: 60/194,614
/ PRIOR FILING DATE: 2000-04-05
/ PRIOR APPLICATION NUMBER: 60/195,063
/ PRIOR FILING DATE: 2000-04-06
/ PRIOR APPLICATION NUMBER: 60/195,066
/ PRIOR FILING DATE: 2000-04-06
/ PRIOR APPLICATION NUMBER: 60/195,067
/ PRIOR FILING DATE: 2000-04-06
/ PRIOR APPLICATION NUMBER: 60/195,068
/ PRIOR FILING DATE: 2000-04-06
/ PRIOR APPLICATION NUMBER: 60/195,069
/ PRIOR FILING DATE: 2000-04-06
/ PRIOR APPLICATION NUMBER: 60/195,070
/ PRIOR FILING DATE: 2000-04-06
/ PRIOR APPLICATION NUMBER: 60/195,510
/ PRIOR FILING DATE: 2000-04-06
/ PRIOR APPLICATION NUMBER: 60/219,855
/ PRIOR FILING DATE: 2000-07-21
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 186
/ SOFTWARE: CuraSeqLast version 0.1
/ SEQ ID NO 28
/ LENGTH: 578
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-174-333-28

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```

Query Match          98.9%; Score 2957.5; DB 15; Length 578;
Best Local Similarity 99.5%; Pred. No. 1e-250;
Matches 575; Conservative 0; Mismatches 0; Indels 3; Gaps 3;

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QY 1 MSODTKVKTSSPPAPSKA-RKLLPVLDPSGDYYWMLNTMVPVWYNLIIVCRACFP 59
DB 1 MSODTKVKTSSPPAPSKARKKLPLVLDPSGDYYWMLNTMVPVWYNLIIVCRACFP 60
QY 60 DLQGYLVAMLVLDYSDLLYLDMVVRFFHT-GFLQGIIVVDGRISSRRVRTWMSFELD 118
DB 61 DLQGYLVAMLVLDYSDLLYLDMVVRFFHTGFLQGIIVVDGRISSRRVRTWMSFELD 120
QY 119 LASLMPDVVVYVRLGPHPTLRLNRLAPRLFEAFRTETRTIYPPAFAIAKMLYIFV 178
DB 121 LASLMPDVVVYVRLGPHPTLRLNRLAPRLFEAFRTETRTIYPPAFAIAKMLYIFV 180
QY 179 VIHNSCLYFALSYRLGFGDAMVYPPDPAQGFRLRQYLYSFYSTLITTVGDTTTP 238
DB 181 VIHNSCLYFALSYRLGFGDAMVYPPDPAQGFRLRQYLYSFYSTLITTVGDTTTP 240
QY 239 ARBEYFLPMVGDFLAVMGFATIMGSSSVIYNNNTADAAFYPDHALVKYMKLQHYNRK 298
DB 241 ARBEYFLPMVGDFLAVMGFATIMGSSSVIYNNNTADAAFYPDHALVKYMKLQHYNRK 300
QY 299 LERRVIDWYQHLOQNKQNTNEVALLOHLPRLRAEVAVSVHLSTLSRVQIFONCEASLLE 358

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DB 301 LERRVIDWYQHLOQNKQNTNEVALLOHLPRLRAEVAVSVHLSTLSRVQIFONCEASLLE 360
QY 359 ELVVKLOPQYSPGEYVCRKGDIGQEMYIIEGQAVVADGITOYAVLAGLYGEISL 418
DB 361 ELVVKLOPQYSPGEYVCRKGDIGQEMYIIEGQAVVADGITOYAVLAGLYGEISL 420
QY 419 INIK-QMNSGRRTNITSLGSDYLCFSKEDLREVLSEYQAOITMEKREILLKXNK 477
DB 421 INIKQMSGRRTNITSLGSDYLCFSKEDLREVLSEYQAOITMEKREILLKXNK 480
QY 478 LDVNAEAEIALQKTESRLRGDQDDDLQTKFARILAEISSALKIATVIERLEWQTR 537
DB 481 LDVNAEAEIALQKTESRLRGDQDDDLQTKFARILAEISSALKIATVIERLEWQTR 540
QY 538 EWPMEPDLAEADDEGEPEEGTSKDEGRASQEGPGE 575
DB 541 EWPMEPDLAEADDEGEPEEGTSKDEGRASQEGPGE 578

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RESULT 9
US-09-735-932-4
/ Sequence 4, Application US/09735932
/ Patent No. US20020037548A1
/ GENERAL INFORMATION:
/ APPLICANT: GUEGLER, Karl et al
/ TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
/ TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUM AN TRANSPORTER PROTEINS,
/ FILE REFERENCE: CL000663
/ CURRENT FILING DATE: US/09/735,932
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 4
/ LENGTH: 575
/ TYPE: PRT
/ ORGANISM: Rattus norvegicus
US-09-735-932-4

```

```

Query Match          94.0%; Score 2811; DB 9; Length 575;
Best Local Similarity 93.4%; Pred. No. 7.7e-238;
Matches 537; Conservative 16; Mismatches 22; Indels 0; Gaps 0;

```

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QY 1 MSODTKVKTSSPPAPSKARKKLPLVLDPSGDYYWMLNTMVPVWYNLIIVCRACFP 60
DB 1 MSODTKVKTSSPPAPSKARKKLPLVLDPSGDYYWMLNTMVPVWYNLIIVCRACFP 60
QY 61 LQHSYLVAMLVLDYSDLLYLDMVVRFFHTGFLQGIIVVDGRISSRRVRTWMSFELD 120
DB 61 LQHSYLVAMLVLDYSDLLYLDMVVRFFHTGFLQGIIVVDGRISSRRVRTWMSFELD 120
QY 121 SLMPDVVVYVRLGPHPTLRLNRLAPRLFEAFRTETRTIYPPAFAIAKMLYIFV 180
DB 121 SLMPDVVVYVRLGPHPTLRLNRLAPRLFEAFRTETRTIYPPAFAIAKMLYIFV 180
QY 181 HNNSCLYFALSYRLGFGDAMVYPPDPAQGFRLRQYLYSFYSTLITTVGDTTTP 240
DB 181 HNNSCLYFALSYRLGFGDAMVYPPDPAQGFRLRQYLYSFYSTLITTVGDTTTP 240
QY 241 EBEYFLPMVGDFLAVMGFATIMGSSSVIYNNNTADAAFYPDHALVKYMKLQHYNRK 300
DB 241 EBEYFLPMVGDFLAVMGFATIMGSSSVIYNNNTADAAFYPDHALVKYMKLQHYNRK 300
QY 301 RRVVIDWYQHLOQNKQNTNEVALLOHLPRLRAEVAVSVHLSTLSRVQIFONCEASLLE 360
DB 301 RRVVIDWYQHLOQNKQNTNEVALLOHLPRLRAEVAVSVHLSTLSRVQIFONCEASLLE 360
QY 361 VLKLOPQYSPGEYVCRKGDIGQEMYIIEGQAVVADGITOYAVLAGLYGEISL 420
DB 361 VLKLOPQYSPGEYVCRKGDIGQEMYIIEGQAVVADGITOYAVLAGLYGEISL 420
QY 421 IKGNSGRRTNITSLGSDYLCFSKEDLREVLSEYQAOITMEKREILLKXNK 480

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Db 421 IKGNNNGNRRTANIKSLGYSDFCLSKEDLREVLSEYPOQAAMEKREILLKNNKLDV 480
QY 481 NAAEAIALQEAATESRLGLDQDDLOTKFARLLAELESSALKIAYRIERLEWQTRWP 540
Db 481 NAAEAIALQEAATESRLGLDQDDLOTKFARLLAELESSALKIAYRIERLEWQTRWP 540
QY 541 MPEDLAADDEGEPEEGTSKDEGRASQEGPPGPE 575
Db 541 MPEDWGEADDEAEPEEGTSKDEGRAGAGPSGIE 575

RESULT 10

US-09-927-267-16
; Sequence 16, Application US/09927267
; Publication No. US20020182691A1
; GENERAL INFORMATION:
; APPLICANT: Creech, Christopher D.
; APPLICANT: Jegla, Timothy J.
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: CNG2B: A No. US20020182691A1 Human Cyclic Nucleotide-Gated Ion
; TITLE OF INVENTION: Channel
; FILE REFERENCE: 018512-006510US
; CURRENT APPLICATION NUMBER: US/09/927,267
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/226,253
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 16
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: rat cyclic nucleotide gated cation channel OCN2
US-09-927-267-16

Query Match 94.0%; Score 2811; DB 9; Length 575;
Best Local Similarity 93.4%; Pred. No. 7,7e-238;
Matches 537; Conservative 16; Mismatches 22; Indels 0; Gaps 0;

QY 1 MSQDTRKVTSSPPAPSAARKLLPYLDPSGDIYVWMLTWPVPMYNIILVCRACFPD 60
Db 1 MSQDQKVTSTSTPPAPSAARKLLPYLDPSGDIYVWMLTWPVPMYNIILVCRACFPD 60
QY 61 LQHGIVLAVLVLDYSDLLYLDMVRFHTGFLGQIILVNDGRSSRVVWSPFLDIA 120
Db 61 LQHGIVLAVLVLDYSDLLYLDMVRFHTGFLGQIILVNDGRSSRVVWSPFLDIA 120
QY 121 SIMPTDVVVRIGPPTPLRLNRFAPLFAFDRTETRTAVPNAFRIAKMLYFVVI 180
Db 121 SIMPTDVVVRIGPPTPLRLNRFAPLFAFDRTETRTAVPNAFRIAKMLYFVVI 180
QY 181 HNSNCLYFALSRYLFGGRDAMVYPDAQGFELRRQVLYSFYFSTLITTVGDPFPPAR 240
Db 181 HNSNCLYFALSRYLFGGRDAMVYPDAQGFELRRQVLYSFYFSTLITTVGDPFPPAR 240
QY 241 EEEYLFMVGDPLLAWGFATIMGSMSSVYNNMTADAAYPPHALYKTKMLQHVNRKE 300
Db 241 EEEYLFMVGDPLLAWGFATIMGSMSSVYNNMTADAAYPPHALYKTKMLQHVNRKE 300
QY 301 RRVIMVYQHLQINKKTNVAILQHLPERLRAEVAVSVHLSTLSRQVIFONCEASLLEEL 360
Db 301 RRVIMVYQHLQINKKTNVAILQHLPERLRAEVAVSVHLSTLSRQVIFONCEASLLEEL 360
QY 361 VLKLPQTVSPBRYVCRKDDIGQEMYIIRGQLAVVADGITOYAVLAGLYFGEISIN 420
Db 361 VLKLPQTVSPBRYVCRKDDIGQEMYIIRGQLAVVADGITOYAVLAGLYFGEISIN 420
QY 421 IKGNNNGNRRTANIKSLGYSDFCLSKEDLREVLSEYPOQAAMEKREILLKNNKLDV 480
Db 421 IKGNNNGNRRTANIKSLGYSDFCLSKEDLREVLSEYPOQAAMEKREILLKNNKLDV 480
QY 481 NAAEAIALQEAATESRLGLDQDDLOTKFARLLAELESSALKIAYRIERLEWQTRWP 540

Db 481 NAAEAIALQEAATESRLGLDQDDLOTKFARLLAELESSALKIAYRIERLEWQTRWP 540
QY 541 MPEDLAADDEGEPEEGTSKDEGRASQEGPPGPE 575
Db 541 MPEDWGEADDEAEPEEGTSKDEGRAGAGPSGIE 575

RESULT 11

US-09-842-758-74
; Sequence 74, Application US/09842758
; Publication No. US20030083244A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A. M.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Zernusen, Bryan D.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Majumder, Kunud
; APPLICANT: Tchernav, Vellizar T.
; APPLICANT: Padigarau, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Gangoli, Esba A.
; APPLICANT: Smithson, Glenda
; APPLICANT: Rastelli, Luca
; APPLICANT: MacDougall, John R.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Groesse, William M.
; APPLICANT: Edward, Szekeres S.
; APPLICANT: Alsobrook II, John P.
; TITLE OF INVENTION: No. US20030083244A1 Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-783
; CURRENT APPLICATION NUMBER: US/09/842,758
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/200,158
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 60/200,613
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,780
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/201,006
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/201,007
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/201,236
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/201,238
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/201,186
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 60/201,474
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/201,508
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/220,591
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: 60/232,678
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 60/263,217
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: 60/265,160
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 74
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-842-758-74

```

Query Match      94.0%; Score 2811; DB 10; Length 575;
Best Local Similarity 93.4%; Pred. No. 7,7e-238;
Matches 537; Conservative 16; Mismatches 22; Indels 0; Gaps 0;

QY 1 MSODTKKTTSESSPPAPSKARKLLPVLDPSGDYYYMMNTMVPVYNNLIIVCRACFPD 60
DB 1 MSODGKVKTTSESTPPATKARKWLPVLDPSGDYYYMMNTMVPVYNNLIIVCRACFPD 60
QY 61 LQHGVLVAMVLVLYTSDLYLDMVVRPHTGFLEOGILVVDKGRISRYRTWSFLDLA 120
DB 61 LQHSYLAVAMFVLDYTDLYLIDIGVRFHTGFLEOGILVVDKGRISRYRTWSFLDLA 120
QY 121 SLMPDVVYVRLGPHPTPLRLNPLRPAFLFEAFDRTESTRAYPNAFRIAKMLYIFVYI 180
DB 121 SLVPTDAAAYVOLGPHIPTLRNLNPLRPAFLFEAFDRTESTRAYPNAFRIAKMLYIFVYI 180
QY 181 HNSCLYFALSRVLGGRDAWVYPPDAOPGFEBRLRQYLYSFFESTLITTVGDTPLPPAR 240
DB 181 HNSCLYFALSRVLGGRDAWVYPPDAOPGFEBRLRQYLYSFFESTLITTVGDTPLPPAR 240
QY 241 EEEYLFMVGDPLLAVMGFATIMGSMSSVYNNMTADAAPYPPHALVKYMKLQHVNRKLE 300
DB 241 EEEYLFMVGDPLLAVMGFATIMGSMSSVYNNMTADAAPYPPHALVKYMKLQHVNRKLE 300
QY 301 RRVIVMYOHLQINKKMTNEVALIOHLPEFLRAEVAVSVHLSLTSRVQIFQNCESLLEEL 360
DB 301 RRVIVMYOHLQINKKMTNEVALIOHLPEFLRAEVAVSVHLSLTSRVQIFQNCESLLEEL 360
QY 361 VKLQOPQYSPGEYVCRKDGIGOEYIIREGOLAVVADGIGQYAVLGAGLYFGESLITN 420
DB 361 VKLQOPQYSPGEYVCRKDGIGOEYIIREGOLAVVADGIGQYAVLGAGLYFGESLITN 420
QY 421 IKGNSGNRRNTANIKSLGYSDLFCLSKEDLREVLSEYPOAQTIMEKGRILLKNNKLDV 480
DB 421 IKGNSGNRRNTANIKSLGYSDLFCLSKEDLREVLSEYPOAQTIMEKGRILLKNNKLDV 480
QY 481 NAEAEIALOEAETESRLGDOOLDLQTKPARLAEBSALKIAYRIERLEWOTRMP 540
DB 481 NAEAEIALOEAETESRLGDOOLDLQTKPARLAEBSALKIAYRIERLEWOTRMP 540
QY 541 MEEDLAEADDEGEPEEGTSKDEGRASOEGPPGPE 575
DB 541 MEEDWGEADDEBAEPGEGTSKDEGRASOEGPBGIE 575

```

RESULT 12
US-10-174-333-74

```

; Sequence 74, Application US/10174333
; Publication No. US20040029220A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Majumder, Kunud
; APPLICANT: Tchiernev, Velizar T.
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Paturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Gangolli, Esna A.
; APPLICANT: Smithson, Glenda
; APPLICANT: Rastelli, Luca
; APPLICANT: MacDougall, John R.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Grose, William M.
; APPLICANT: Szekeres, Edward S.
; APPLICANT: Alebrook, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Guo, Xiaojia (Sasha)

```

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; APPLICANT: Li, Li
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-783 CIP1
; CURRENT APPLICATION NUMBER: US/10/174,333
; PRIOR FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 60/193,664
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/194,614
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 60/195,063
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,066
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,067
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,068
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,069
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,070
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,510
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/219,855
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: Cursedq1st version 0.1
; SEQ ID NO 74
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; US-10-174-333-74

```

```

Query Match      94.0%; Score 2811; DB 15; Length 575;
Best Local Similarity 93.4%; Pred. No. 7,7e-238;
Matches 537; Conservative 16; Mismatches 22; Indels 0; Gaps 0;

```

```

QY 1 MSODTKKTTSESSPPAPSKARKLLPVLDPSGDYYYMMNTMVPVYNNLIIVCRACFPD 60
DB 1 MSODGKVKTTSESTPPATKARKWLPVLDPSGDYYYMMNTMVPVYNNLIIVCRACFPD 60
QY 61 LQHGVLVAMVLVLYTSDLYLDMVVRPHTGFLEOGILVVDKGRISRYRTWSFLDLA 120
DB 61 LQHSYLAVAMFVLDYTDLYLIDIGVRFHTGFLEOGILVVDKGRISRYRTWSFLDLA 120
QY 121 SLMPDVVYVRLGPHPTPLRLNPLRPAFLFEAFDRTESTRAYPNAFRIAKMLYIFVYI 180
DB 121 SLVPTDAAAYVOLGPHIPTLRNLNPLRPAFLFEAFDRTESTRAYPNAFRIAKMLYIFVYI 180
QY 181 HNSCLYFALSRVLGGRDAWVYPPDAOPGFEBRLRQYLYSFFESTLITTVGDTPLPPAR 240
DB 181 HNSCLYFALSRVLGGRDAWVYPPDAOPGFEBRLRQYLYSFFESTLITTVGDTPLPPAR 240
QY 241 EEEYLFMVGDPLLAVMGFATIMGSMSSVYNNMTADAAPYPPHALVKYMKLQHVNRKLE 300
DB 241 EEEYLFMVGDPLLAVMGFATIMGSMSSVYNNMTADAAPYPPHALVKYMKLQHVNRKLE 300
QY 301 RRVIVMYOHLQINKKMTNEVALIOHLPEFLRAEVAVSVHLSLTSRVQIFQNCESLLEEL 360
DB 301 RRVIVMYOHLQINKKMTNEVALIOHLPEFLRAEVAVSVHLSLTSRVQIFQNCESLLEEL 360
QY 361 VKLQOPQYSPGEYVCRKDGIGOEYIIREGOLAVVADGIGQYAVLGAGLYFGESLITN 420
DB 361 VKLQOPQYSPGEYVCRKDGIGOEYIIREGOLAVVADGIGQYAVLGAGLYFGESLITN 420
QY 421 IKGNSGNRRNTANIKSLGYSDLFCLSKEDLREVLSEYPOAQTIMEKGRILLKNNKLDV 480
DB 421 IKGNSGNRRNTANIKSLGYSDLFCLSKEDLREVLSEYPOAQTIMEKGRILLKNNKLDV 480
QY 481 NAEAEIALOEAETESRLGDOOLDLQTKPARLAEBSALKIAYRIERLEWOTRMP 540
DB 481 NAEAEIALOEAETESRLGDOOLDLQTKPARLAEBSALKIAYRIERLEWOTRMP 540

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Db 481 NAAEALQEAATESRLKGLDQDLQTKFARLLAELESSALKIAYRIERLEWQREMP 540
 QY 541 MEDLADEGEPEEGTSGKEGRASQEGPPGE 575
 Db 541 MEDMGADDEAPEEGTSGKEGRAGQAGPSGIE 575

RESULT 13
 US-10-207-951-4
 ; Sequence 4, Application US/10207951
 ; Publication No. US20030013156A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KARL GUEGLER et al.
 ; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS
 ; TITLE OF INVENTION: AND USES THEREOF
 ; FILE REFERENCE: CLO0063CON
 ; CURRENT APPLICATION NUMBER: US/10/207,951
 ; PRIOR FILING DATE: 2002-07-31
 ; PRIOR APPLICATION NUMBER: 09/735,932
 ; PRIOR FILING DATE: 2000-12-14
 ; PRIOR APPLICATION NUMBER: 60/211,223
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 1704
 ; TYPE: PRT
 ; ORGANISM: Rattus norvegicus
 US-10-207-951-4

Query Match 80.1%; Score 2394; DB 14; Length 1704;
 Best Local Similarity 37.1%; Pred No. 1.8e-200;
 Matches 567; Conservative 5; Mismatches 3; Indels 952; Gaps 9;

QY 1 MSQDTKVTTESSPPAPSKARKLLPYLDSGDYYWMLNTWFPVWYNLIILVCRACFPD 60
 Db 117 MSQDKVKTTSTPAPTKARKMLPYLDSGDYYWMLNTWFPVWYNLIIVCRACFPD 176
 QY 61 -LQHGIVAMLVLDYTSDDLILDMVVRHTGFLBQGLIVVDKGRSSRYVWTSGFLDL 119
 Db 177 QLOHGIVAMLVLDYTSDDLILDMVVRHTGFLBQGLIVVDKGRSSRYVWTSGFLDL 236
 QY 120 A----- 120
 Db 237 ALQHTLVAMVLDYTSDDLILDMVVRHTGFLBQGLIVVDKGRSSRYVWTSGFLDLASQHSY 296
 QY 121 -----SLMP 124
 Db 297 LVAMFVLDTSDLVLLDIGVRFHGFLEQGLIVVDKGMIASRYVWTSGFLDLAQSLMP 356
 QY 135 TVVVYVRLGPHPTTLRLNRLFLRFLFEAFDRTETRTAYPNAFRIAKMLYIFVYI---- 180
 Db 357 TVVVYVRLGPHPTTLRLNRLFLRFLFEAFDRTETRTAYPNAFRIAKMLYIFVYISLPT 416
 QY 181 ----- 180
 Db 417 DYVLGPHPTTLRLNRLFLRFLFEAFDRTETRTAYPNAFRIAKMLYIFVYISSIVPTDAY 476
 QY 181 -----HMNSCLYF 188
 Db 477 VOLGPHPTTLRLNRLFLRFLFEAFDRTETRTAYPNAFRIAKMLYIFVYIHMNSCLYF 536
 QY 189 ALSRYLGFGRDAMVYDPAQPGFERLRQYLYSFYSTLILTTVGDTPPRSHNSCLYFA 240
 Db 537 ALSRYLGFGRDAMVYDPAQPGFERLRQYLYSFYSTLILTTVGDTPPPARHNSCLYF 596
 QY 241 ----- 240
 Db 597 ALSRYLGFGRDAMVYDPAQPGFERLRQYLYSFYSTLILTTVGDTPPRSHNSCLYFA 656
 QY 241 -----EEEYLFMV 248
 |||||

Db 657 LSRYLGFGRDAMVYDPAQPGFERLRQYLYSFYSTLILTTVGDTPPROEEBYLFMV 716
 QY 249 GDFLLAVMGFATIMGSMSSVIYNNMTADAAFYPDHALVKYMKLOHVNLESEEEYLFMV 300
 Db 717 GDFLLAVMGFATIMGSMSSVIYNNMTADAAFYPDHALVKYMKLOHVNRLKEEYLFMV 776
 QY 301 ----- 300
 Db 777 GDFLLAVMGFATIMGSMSSVIYNNMTADAAFYPDHALVKYMKLOHVNLESEEEYLFMV 836
 QY 301 ----- 300
 Db 837 DFLAVMGFATIMGSMSSVIYNNMTADAAFYPDHALVKYMKLOHVNRLKEEYLFMV 896
 QY 301 ----- 300
 Db 897 HLQINKKMSNEVALIQHLPERLRAEVAVSVHLSTLSRVOIFQNCASLLEELRVIDWYQ 956
 QY 301 -----RVIDWYQ 308
 Db 957 HLQINKKMSNEVALIQHLPERLRAEVAVSVHLSTLSRVOIFQNCASLLEELRVIDWYQ 1016
 QY 309 HLQINKKMTNEVALIQHLPERLRAEVAVSVHLSTLSRVOIFQNCASLLEEL-VLKLPQ 367
 Db 1017 HLQINKKMTNEVALIQHLPERLRAEVAVSVHLSTLSRVOIFQNCASLLEELQVLKLPQ 1076
 QY 368 TYPGEYVCRKGDIGQEMYIIREGQAVVADDTQYAVLAGLYFGESIIIN----- 420
 Db 1077 TYPGEYVCRKGDIGQEMYIIREGQAVVADDTQYAVLAGLYFGESIIINVLKLPQ 1136
 QY 421 ----- 420
 Db 1137 TYPGEYVCRKGDIGQEMYIIREGQAVVADDTQYAVLAGLYFGESIIINVLKLPQ 1196
 QY 421 ----- 420
 Db 1197 YSPGEYVCRKGDIGREMYIIREGQAVVADDTQYAVLAGLYFGESIIINQIKGNSG 1256
 QY 421 ----- 420
 Db 1257 NRRTNISLGSYDLFCLSKEDLREVLSEYPOAQIMEKGREILLKMSKLDVIGKNSG 1316
 QY 421 -----IKGNSGNR 430
 Db 1317 NRRTNISLGSYDLFCLSKEDLREVLSEYPOAQIMEKGREILLKMSKLDVIGKNSGNR 1376
 QY 431 TANISLGSYDLFCLSKEDLREVLSEYPOAQIMEKGREILLKMSKLDV-NAAEAETAL 489
 Db 1377 TANISLGSYDLFCLSKEDLREVLSEYPOAQIMEKGREILLKMSKLDVQNAEAETAL 1436
 QY 490 QEAATESRLKGLDQDLQTKFARLLAELESSALKIAYRIERLEWQREMP----- 540
 Db 1437 QEAATESRLKGLDQDLQTKFARLLAELESSALKIAYRIERLEWQREMPNAAEAETAL 1496
 QY 541 ----- 540
 Db 1497 QEAATESRLKGLDQDLQTKFARLLAELESSALKIAYRIERLEWQREMPNAAEAETAL 1556
 QY 541 -----MEDLAEA 548
 Db 1557 QEAATESRLKGLDQDLQTKFARLLAELESSALKIAYRIERLEWQREMPMEDLAEA 1616
 QY 549 DDEGPEEGTSGKEGRASQEGPPGE 575
 Db 1617 DDEGPEEGTSGKEGRASQEGPPGE 1643

RESULT 14
 US-10-029-677-16
 ; Sequence 16, Application US/10029677
 ; Publication No. US20030096249A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Westphal, Ryan S.

```

? APPLICANT: Feder, John N.
? APPLICANT: Ramanaathan, Chandra S.
? APPLICANT: Mintlier, Gabriel A.
? TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND POLYPEPTIDES FOR A HUMAN CATION CHANNEL
? TITLE OF INVENTION: POLYPEPTIDE
? FILE REFERENCE: D0187NP
? CURRENT APPLICATION NUMBER: US/10/029,677
? CURRENT FILING DATE: 2002-05-06
? PRIOR APPLICATION NUMBER: US 60/257,865
? PRIOR FILING DATE: 2000-12-21
? NUMBER OF SEQ ID NOS: 24
? SOFTWARE: PatentIn version 3.0
? SEQ ID NO 16
? LENGTH: 663
? TYPE: PRT
? ORGANISM: Bos taurus
US-10-029-677-16

Query March 52.5%; Score 1568; DB 14; Length 663;
Best Local Similarity 54.2%; Pred. No. 1.7e+28;
Matches 292; Conservative 108; Mismatches 133; Indels 6; Gaps 2;

```


XX WPI: 2002-315109/35.
 DR N-PSDB; AAD33869.
 XX
 PT Nucleic acids encoding cyclic nucleotide-gated ion channel subfamily
 PT transporter proteins (Tpe), useful in prevention, diagnosis and treatment
 PT of TP-related diseases.
 XX
 PS Claim 1; Fig 2; 45pp; English.
 CC
 CC The invention relates to nucleic acid sequences that encode protein
 CC molecules which are members of the transporter family of proteins and are
 CC related to the cyclic nucleotide-gated ion channel subfamily. The
 CC transporter protein DNA may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate transporter protein
 CC expression. Transporter protein and its DNA are used to treat disorders
 CC associated with decreased transporter protein expression by rectifying
 CC mutations or deletions in a patient's genome that affect the activity of
 CC the transporter proteins by expressing inactive proteins or to supplement
 CC the patients own production of them. Transporter protein DNA and its
 CC complementary sequences may also be used in gene therapy and as DNA
 CC probes in diagnostic assays and to detect and quantitate the presence of
 CC similar nucleic acids in samples, and therefore which patients may be in
 CC need of restorative therapy. They may also be used in the production of
 CC transgenic animals in which transporter protein expression and activity
 CC may be studied. Transporter protein is useful in protein therapy and in
 CC the production of vaccines. The present sequence is human transporter
 CC protein. Human transporter protein gene is located on chromosome 11
 XX
 XX Sequence 575 AA;
 SQ

Query Match 100.0%; Score 2989; DB 5; Length 575;
 Best Local Similarity 100.0%; Pred. No. 8.7e-278;
 Matches 575; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQDTKVKTTSSPPAPSKARKLLPVLDPSSGYYWMLNTWVPMYNIILVCRACFPD 60
 DB 1 MSQDTKVKTTSSPPAPSKARKLLPVLDPSSGYYWMLNTWVPMYNIILVCRACFPD 60
 QY 61 LQHGIVAMLVLDYSDLLYLDMVVRFTGFLGEGILVVDKGRISRRVYRTWSFFLDA 120
 DB 61 LQHGIVAMLVLDYSDLLYLDMVVRFTGFLGEGILVVDKGRISRRVYRTWSFFLDA 120
 QY 121 SLMPDQVYVRLGPHPTFLRLRFLAPLFEAFDSTETRTAEPNAPRIAKMLYIFVVI 180
 DB 121 SLMPDQVYVRLGPHPTFLRLRFLAPLFEAFDSTETRTAEPNAPRIAKMLYIFVVI 180
 QY 121 SLMPDQVYVRLGPHPTFLRLRFLAPLFEAFDSTETRTAEPNAPRIAKMLYIFVVI 180
 DB 121 SLMPDQVYVRLGPHPTFLRLRFLAPLFEAFDSTETRTAEPNAPRIAKMLYIFVVI 180
 QY 181 HNSCLYFALSRYLGFGRDAMVYPDPAQGFELRRQVLYSPFSTLILTTVGDTPPAP 240
 DB 181 HNSCLYFALSRYLGFGRDAMVYPDPAQGFELRRQVLYSPFSTLILTTVGDTPPAP 240
 QY 181 HNSCLYFALSRYLGFGRDAMVYPDPAQGFELRRQVLYSPFSTLILTTVGDTPPAP 240
 DB 181 HNSCLYFALSRYLGFGRDAMVYPDPAQGFELRRQVLYSPFSTLILTTVGDTPPAP 240
 QY 241 EBEYLFMVDGFLAVWGFATIMSGSVYNNMTADAAFPDHALYKTKLQHVNRKLE 300
 DB 241 EBEYLFMVDGFLAVWGFATIMSGSVYNNMTADAAFPDHALYKTKLQHVNRKLE 300
 QY 241 EBEYLFMVDGFLAVWGFATIMSGSVYNNMTADAAFPDHALYKTKLQHVNRKLE 300
 DB 241 EBEYLFMVDGFLAVWGFATIMSGSVYNNMTADAAFPDHALYKTKLQHVNRKLE 300
 QY 301 RRVYIDYQHLQIKKMTNEVALIQHLPRLRAVAASVHLSTSRVQIFONCEASLLEEL 360
 DB 301 RRVYIDYQHLQIKKMTNEVALIQHLPRLRAVAASVHLSTSRVQIFONCEASLLEEL 360
 QY 301 RRVYIDYQHLQIKKMTNEVALIQHLPRLRAVAASVHLSTSRVQIFONCEASLLEEL 360
 DB 301 RRVYIDYQHLQIKKMTNEVALIQHLPRLRAVAASVHLSTSRVQIFONCEASLLEEL 360
 QY 361 VLKQPTQYSPGEYVCRKDDIGEMYIIRGQLAVVADGITQYAVLAGLYGEISIIIN 420
 DB 361 VLKQPTQYSPGEYVCRKDDIGEMYIIRGQLAVVADGITQYAVLAGLYGEISIIIN 420
 QY 421 IKGNMGNRRNTANIKSLGYSDFLCLSKEDLREVLSEYPOAQITMEKGRILLKXKLV 480
 DB 421 IKGNMGNRRNTANIKSLGYSDFLCLSKEDLREVLSEYPOAQITMEKGRILLKXKLV 480
 QY 421 IKGNMGNRRNTANIKSLGYSDFLCLSKEDLREVLSEYPOAQITMEKGRILLKXKLV 480
 DB 421 IKGNMGNRRNTANIKSLGYSDFLCLSKEDLREVLSEYPOAQITMEKGRILLKXKLV 480
 QY 481 NAEAAITAOEATESLRLGDDQDLQOTKFAFLLEBESSALKIYRIERLEWQTRMP 540
 DB 481 NAEAAITAOEATESLRLGDDQDLQOTKFAFLLEBESSALKIYRIERLEWQTRMP 540
 QY 541 MPEDLAADDEGEPEEGTSKDEGRASQEGPPGPE 575
 DB 541 MPEDLAADDEGEPEEGTSKDEGRASQEGPPGPE 575

DB 541 MPEDLAADDEGEPEEGTSKDEGRASQEGPPGPE 575

RESULT 3
 ABB07725
 ID ABB07725 standard; protein; 575 AA.
 XX
 AC ABB07725;
 XX
 DT 10-JUN-2002 (first entry)
 XX
 DE Human cyclic nucleotide-gated cation channel subunit, CNG2B.
 XX
 KW Cyclic nucleotide-gated cation channel; CNG2B; CNG; cation channel;
 KW cyclic nucleotide-gating; neuroprotective; cytostatic; antiviral;
 KW gene therapy; human.
 XX
 OS Homo sapiens.
 XX
 PN WO200214467-A2.
 XX
 PD 21-FEB-2002.
 XX
 PF 13-AUG-2001; 2001WO-US0253392.
 XX
 PR 17-AUG-2000; 2000US-0226253P.
 PR 10-AUG-2001; 2001US-00927267.
 XX
 PA (ICAG-) ICAGEN INC.
 XX
 PI Creech CD, Jegla TJ;
 XX
 DR WPI: 2002-269183/31.
 DR N-PSDB; ABA95279; ABA95280.
 XX
 PT New cyclic nucleotide gated cation channel nucleic acids, useful in gene
 PT therapy for correcting acquired and inherited genetic defects, cancer and
 PT viral infection.
 XX
 PS Claim 15; Fig 4; 78pp; English.
 CC
 CC The invention relates to a novel human cyclic nucleotide-gated cation
 CC channel subunit, CNG2B. The polypeptide forms with at least one cyclic
 CC nucleotide gated cation channel (CNG) alpha subunit, a cation channel
 CC having the characteristic of cyclic nucleotide-gating. CNG2B polypeptides
 CC are useful for testing inhibitors and activators of cyclic nucleotide-
 CC gated cation channels, where such activators or inhibitors are useful as
 CC pharmaceutical agents for treating diseases involving abnormal ion flux,
 CC e.g. neurological disorders. CNG2B nucleic acids and polypeptides are
 CC also useful for diagnostic applications for diseases involving abnormal
 CC ion flux. CNG2B genes may be used in gene therapy to correct acquired and
 CC inherited genetic defects, cancer and viral infection. CNG2B can be used
 CC as an indicator of current flow in a particular direction, or as an
 CC indirect reporter via attachment to a second reporter molecule, such as
 CC green fluorescent protein. CNG2B modulators are useful for treating neu
 CC logical diseases. The present sequence represents the human CNG2B
 XX
 XX Sequence 575 AA;
 SQ

Query Match 100.0%; Score 2989; DB 5; Length 575;
 Best Local Similarity 100.0%; Pred. No. 8.7e-278;
 Matches 575; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQDTKVKTTSSPPAPSKARKLLPVLDPSSGYYWMLNTWVPMYNIILVCRACFPD 60
 DB 1 MSQDTKVKTTSSPPAPSKARKLLPVLDPSSGYYWMLNTWVPMYNIILVCRACFPD 60
 QY 61 LQHGIVAMLVLDYSDLLYLDMVVRFTGFLGEGILVVDKGRISRRVYRTWSFFLDA 120
 DB 61 LQHGIVAMLVLDYSDLLYLDMVVRFTGFLGEGILVVDKGRISRRVYRTWSFFLDA 120
 QY 121 SLMPDQVYVRLGPHPTFLRLRFLAPLFEAFDSTETRTAEPNAPRIAKMLYIFVVI 180
 DB 121 SLMPDQVYVRLGPHPTFLRLRFLAPLFEAFDSTETRTAEPNAPRIAKMLYIFVVI 180

Db	121	SLMPTDVVYVRLGPHPTLRLNRLRAPRLFEAFDRTETRTAYPNARLAKMLYIFVVI	180
Qy	181	HMNSCLYFALSRYLGFGRDAMVYPPDPAOPGEERLROXYLSFYSTLILTTVGDTTPPAR	240
Db	181	HMNSCLYFALSRYLGFGRDAMVYPPDPAOPGEERLROXYLSFYSTLILTTVGDTTPPAR	240
Qy	241	EEBYLFVWGDPLLAVMGFATIMSGSSVINYMTADAAFPDHALVKKYMKLOHVNRKLE	300
Db	241	EEBYLFVWGDPLLAVMGFATIMSGSSVINYMTADAAFPDHALVKKYMKLOHVNRKLE	300
Qy	301	RRVIDWYOHQINKNKMTNEVALIIOHLPERLRAVAVSVHLSTLSRVQIFONCEASLLEEL	360
Db	301	RRVIDWYOHQINKNKMTNEVALIIOHLPERLRAVAVSVHLSTLSRVQIFONCEASLLEEL	360
Qy	361	VLKLPQYTPSPGSEYVCKRGDIGEMYYIREGOLAVVADGITOYAVLAGAGLYFGEISIN	420
Db	361	VLKLPQYTPSPGSEYVCKRGDIGEMYYIREGOLAVVADGITOYAVLAGAGLYFGEISIN	420
Qy	421	IKGNMGNRRNTANIKSLGYSDLFCLSKEDLREVLSEYPOAQITMEKREIILKNKCLDV	480
Db	421	IKGNMGNRRNTANIKSLGYSDLFCLSKEDLREVLSEYPOAQITMEKREIILKNKCLDV	480
Qy	481	NAEAAEIALQEAATESRLRGDQDLDTQTKFARLLAELESSALKIAYRIERLEWQTRMP	540
Db	481	NAEAAEIALQEAATESRLRGDQDLDTQTKFARLLAELESSALKIAYRIERLEWQTRMP	540
Qy	541	MPEDLAADDEGEPEEGTSKDEGRASOGPPGPE	575
Db	541	MPEDLAADDEGEPEEGTSKDEGRASOGPPGPE	575
RESULT 4			
ABU09091			
ID	ABU09091	standard, protein; 575 AA.	
AC	ABU09091;		
DT	05-AUG-2003	(first entry)	
DE		Human transporter polypeptide.	
KM		Human; transporter.	
OS		Homo sapiens.	
FH		Key	
FT	Misc-difference	317	location/Qualifiers
FT	Misc-difference	432	/note= "Encoded by TCC"
FT	Misc-difference	476	/note= "Encoded by ACC"
FT	Misc-difference	553	/note= "Encoded by AGC"
FT			/note= "Val substituted by Glu"
EN	US2003013156-A1.		
PD	16-JAN-2003.		
PF	31-JUL-2002; 2002US-00207951.		
PR	13-JUN-2000; 2000US-0211223P.		
PR	14-DEC-2000; 2000US-00735932.		
PA	(APPL-) APPLERA CORP.		
PI	Guegler K, Ketchum KA, Di Francesco V, Beasley EM;		
DR	WPI; 2003-416799/39.		
DR	N-PSDB; ABX95978.		
PT		New transporter proteins related to cyclic nucleotide-gated ion channel	
PT		subfamily and polynucleotide encoding the protein for diagnosing,	

PT	treating diseases mediated by transporter protein and identifying
PT	modulators.
XX	Claim 1; Fig 2A; 52pp; English.
PS	
XX	
CC	The invention relates to an isolated human transporter polypeptide and
CC	the polynucleotide encoding it. The polypeptide is useful for identifying
CC	a modulator of the expression of the protein by contacting the protein
CC	with an agent and determining if the agent has modulated the function,
CC	activity or expression of the protein. The agent is administered to a
CC	host cell comprising an expression vector that expresses the protein. The
CC	polypeptide is also useful for identifying an agent that binds to the
CC	transporter protein. The polypeptide or condition mediated by a human
CC	models for the development of human therapeutic targets, to aid in the
CC	identification of therapeutic proteins and to serve as targets for the
CC	development of human therapeutic agents that modulate transporter
CC	activity in cells and tissues that express the transporter. The
CC	polypeptide is useful for raising antibodies or for eliciting another
CC	immune response, as a reagent in assays designed to quantitatively
CC	determine levels of the protein in biological fluids, as markers for
CC	tissues in which the corresponding protein is expressed and to identify
CC	the binding partner/ligand so as to develop a system to identify
CC	inhibitors of the binding interactions. This sequence represents the
CC	human transporter of the invention
CC	
XX	
SO	Sequence 575 AA;
Query Match	100.0%; Score 2989; DB 6; Length 575;
Best Local Similarity	100.0%; Mismatch No. 8; 7e-278;
Matches 575; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 MSODTKVKTSSSPAPSKARKLLPVLDPSGDYTYMMNTMVPWNLIILVCRACFPD 60
Db	1 MSODTKVKTSSSPAPSKARKLLPVLDPSGDYTYMMNTMVPWNLIILVCRACFPD 60
Qy	61 LQHGVLVAMLVLDYSDLLYLDMVVFHFGFLEOGILVVDKGRISRYRTWSFPLDA 120
Db	61 LQHGVLVAMLVLDYSDLLYLDMVVFHFGFLEOGILVVDKGRISRYRTWSFPLDA 120
Qy	121 SLMPTDVVYVRLGPHPTLRLNRLRAPRLFEAFDRTETRTAYPNARLAKMLYIFVVI 180
Db	121 SLMPTDVVYVRLGPHPTLRLNRLRAPRLFEAFDRTETRTAYPNARLAKMLYIFVVI 180
Qy	181 HMNSCLYFALSRYLGFGRDAMVYPPDPAOPGEERLROXYLSFYSTLILTTVGDTTPPAR 240
Db	181 HMNSCLYFALSRYLGFGRDAMVYPPDPAOPGEERLROXYLSFYSTLILTTVGDTTPPAR 240
Qy	241 EEBYLFVWGDPLLAVMGFATIMSGSSVINYMTADAAFPDHALVKKYMKLOHVNRKLE 300
Db	241 EEBYLFVWGDPLLAVMGFATIMSGSSVINYMTADAAFPDHALVKKYMKLOHVNRKLE 300
Qy	301 RRVLDWYOHQINKNKMTNEVALIIOHLPERLRAVAVSVHLSTLSRVQIFONCEASLLEEL 360
Db	301 RRVLDWYOHQINKNKMTNEVALIIOHLPERLRAVAVSVHLSTLSRVQIFONCEASLLEEL 360
Qy	361 VLKLPQYTPSPGSEYVCKRGDIGEMYYIREGOLAVVADGITOYAVLAGAGLYFGEISIN 420
Db	361 VLKLPQYTPSPGSEYVCKRGDIGEMYYIREGOLAVVADGITOYAVLAGAGLYFGEISIN 420
Qy	421 IKGNMGNRRNTANIKSLGYSDLFCLSKEDLREVLSEYPOAQITMEKREIILKNKCLDV 480
Db	421 IKGNMGNRRNTANIKSLGYSDLFCLSKEDLREVLSEYPOAQITMEKREIILKNKCLDV 480
Qy	481 NAEAAEIALQEAATESRLRGDQDLDTQTKFARLLAELESSALKIAYRIERLEWQTRMP 540
Db	481 NAEAAEIALQEAATESRLRGDQDLDTQTKFARLLAELESSALKIAYRIERLEWQTRMP 540
Qy	541 MPEDLAADDEGEPEEGTSKDEGRASOGPPGPE 575
Db	541 MPEDLAADDEGEPEEGTSKDEGRASOGPPGPE 575

RESULT 5	
ABP55141	
ID	ABP55141 standard; protein; 575 AA.
XX	
AC	ABP55141;
XX	
DT	05-FEB-2003 (first entry)
XX	
DE	Human cyclic nucleotide-gated channel OCN2 subunit.
XX	
KW	OCN2; cyclic nucleotide-gated channel; human; cardiovascular disorder;
KW	neurological disorder; cardiac; vasotropic; antiarrhythmic; hypotensive;
KW	neuroprotective; nootropic; gene therapy.
OS	Homo sapiens.
XX	
XX	
Key	Location/Qualifiers
FT	33..51
FT	/note="transmembrane helix"
FT	64..86
FT	/note="transmembrane helix"
FT	172..190
FT	/note="transmembrane helix"
FT	218..236
FT	/note="transmembrane helix"
FT	248..270
FT	/note="transmembrane helix"
FT	375..392
FT	/note="cyclic nucleotide-binding domain signature"
FT	413..437
FT	/note="cyclic nucleotide-binding domain signature"
Domain	
XX	
XX	
XX	WC020281689-A1.
XX	
XX	
PD	17-OCT-2002.
XX	
XX	
PF	19-FEB-2002; 2002MO-EP001726.
XX	
XX	
PR	20-FEB-2001; 2001US-0269402P.
XX	
PR	13-NOV-2001; 2001US-0331227P.
XX	
PR	23-JAN-2002; 2002US-0350038P.
XX	
PA	(FARB) BAYER AG.
XX	
XX	
PI	Zhu Z;
XX	
DR	WPI: 2003-046865/04.
XX	
DR	N-PSDB; ABV75870.
XX	
XX	
PS	Claim 25; Fig 2; 112pp; English.
XX	
CC	The present sequence is the protein sequence of a novel human cyclic
CC	nucleotide-gated channel OCN2 subunit polypeptide, a human orthologue of
CC	rat olfactory cyclic nucleotide-gated channel OCN2 subunit, containing
CC	transmembrane and cyclic nucleotide-binding domains. The invention
CC	provides human OCN2 subunit polynucleotides and polypeptides, methods
CC	for their detection, expression vectors, host cells, and methods of
CC	screening for agents which decrease or regulate the activity of the OCN2
CC	subunit. Claimed pharmaceutical compositions comprise an expression
CC	vector encoding the OCN2 subunit, or comprise a reagent which modulates
CC	the subunit's activity. These are used to treat a cardiovascular disorder
CC	or a central nervous system (CNS) disorder. Agents which modulate an
CC	activity of the OCN2 subunit include antibodies and antisense
CC	oligonucleotides (all claimed). The pharmaceutical compositions are
CC	useful for treating, preventing or ameliorating cardiovascular diseases
CC	such as congestive heart failure, myocardial infarction, ischaemic
CC	diseases of the heart, atrial and ventricular arrhythmias, hypertensive
CC	vascular diseases, and peripheral vascular diseases and to screen for
CC	human cyclic nucleotide-gated channel OCN2 subunit activators and

	Query Match	100.0%	Score 2989	DB 6	Length 575	
	Best Local Similarity	100.0%	Pred. No. 8.7e-278			
	Matches 575	Conservative 0	Mismatches 0	Indels 0	Gaps 0	
XX	Sequence 575 AA:					
QY	1 MSODTKVTTSSPPAPSKARKLLPVLDPSGDYYMMINTWFPVMNLIILVCRACPD					60
DB	1 MSQDTKVTSTSSPPAPSKARKLLPVLDPSGDYYMMINTWFPVMNLIILVCRACPD					60
QY	61 LQHGIVAMLVLDYTSDDLILYLDWVVRPHGFLGEGILVVDKGRISSRVWTSFFLLA					120
DB	61 LQHGIVAMLVLDYTSDDLILYLDWVVRPHGFLGEGILVVDKGRISSRVWTSFFLLA					120
QY	121 SLMPDVVVYVVGHTPTPLRLNRFARARLFEAPRTESTRTPAYPAFPAKMLKYPVYI					180
DB	121 SLMPDVVVYVVGHTPTPLRLNRFARARLFEAPRTESTRTPAYPAFPAKMLKYPVYI					180
QY	181 HNSCLVYALSRVYLGFGDAMVYEDPAQGFESRLROYLYSFYFSTLLITTVGDTPPAR					240
DB	181 HNSCLVYALSRVYLGFGDAMVYEDPAQGFESRLROYLYSFYFSTLLITTVGDTPPAR					240
QY	241 EEEYLFVWGVDFLLAVMGFATIMGSSVYINMNTADAAPYPDHALVKKYMKLOHVRKLE					300
DB	241 EEEYLFVWGVDFLLAVMGFATIMGSSVYINMNTADAAPYPDHALVKKYMKLOHVRKLE					300
QY	301 RRVLDWVOHLOINKKMTNEVALIOLHPLRLAEVAVSVHLSSTLSVQIFONCEASLLEEL					360
DB	301 RRVLDWVOHLOINKKMTNEVALIOLHPLRLAEVAVSVHLSSTLSVQIFONCEASLLEEL					360
QY	361 VLKIQPQYTSGEYVCRKDGIGOEYIIRERQLANVADGITYAVLAGLYFGESIIIN					420
DB	361 VLKIQPQYTSGEYVCRKDGIGOEYIIRERQLANVADGITYAVLAGLYFGESIIIN					420
QY	421 IKGNSGNRRANTIKSLGYSDFCLSKEDLEVLSEYPOAQITIMEKREIILKNKLDV					480
DB	421 IKGNSGNRRANTIKSLGYSDFCLSKEDLEVLSEYPOAQITIMEKREIILKNKLDV					480
QY	481 NAEAAEIALQATSRRLGLDQQLDLOTKARLAELESSALKIAYRIERLEMOTREWP					540
DB	481 NAEAAEIALQATSRRLGLDQQLDLOTKARLAELESSALKIAYRIERLEMOTREWP					540
QY	541 MPEDLAEDDEGEPEEGTSKDDEGRASOEGPPGPE					575
DB	541 MPEDLAEDDEGEPEEGTSKDDEGRASOEGPPGPE					575
RESULT 6						
ADH11623						
ID	ADH11623 standard; protein, 575 AA.					
XX	ADH11623;					
AC	ADH11623;					
XX						
DT	11-MAR-2004 (first entry)					
XX						
DE	Human Hipnum 222 SEQ ID 2.					
XX						
XX						
KW	Human; cyclic nucleotide-gated ion channel; CNG; Hipnum 222;					
KW	chronic obstructive pulmonary disease; COPD; asthma; cough;					
KW	acute bronchitis; acute respiratory failure;					
KW	adult respiratory distress syndrome; cystic fibrosis; emphysema;					
KW	Goodpasture's syndrome; pneumonia; pulmonary embolism; bartoldeis;					
KW	tuberculosis; squamous cell carcinoma; small cell lung carcinoma; testes;					
KW	tubercula; lung; cerebellum; adipose tissue; chromosome 11p15.4;					
KW	antiinflammatory; antiaesthetic; antitussive; nephrotropic; cyostatic;					
KW	thrombolytic; tuberculosis; gene therapy.					
XX						
XX	Homo sapiens.					
XX						

PN GB2379932-A.
 XX 26-MAR-2003.
 XX 20-AUG-2002; 2002GB-00019387.
 XX 22-AUG-2001; 2001GB-00020350.
 XX (GLAX) GLAXO GROUP LTD.
 XX
 PI Crowther D, Powell AJ, Richards CA;
 XX
 XX WPI; 2003-345047/33.
 DR N-PSDB; ADH11622.
 XX
 PT Novel isolated cyclic nucleotide-gated ion channel polypeptide, referred
 PT as Hiphum 222, useful for identifying modulators of cyclic nucleotide-
 PT gated ion channel activity, that are used for treating asthma, cough.
 XX
 PS Claim 1; Page 29; 34pp; English.

CC The present invention relates to an isolated human cyclic nucleotide-
 CC gated (CNG) ion channel polypeptide (Hiphum 222; I. ADH11623) and its
 CC coding sequence (II; ADH11622). Substances which modulate (I) and/or (II)
 CC activity/expression are treating a subject having a disorder that is
 CC responsive to CNG ion channel modulation e.g. chronic obstructive
 CC pulmonary disease (COPD), asthma, cough, acute bronchitis, acute
 CC respiratory failure in COPD, adult respiratory distress syndrome, cystic
 CC fibrosis, emphysema, Goodpasture's syndrome, pneumonia, pulmonary
 CC embolism, sarcoidosis, tuberculosis, squamous cell carcinoma and small
 CC cell lung carcinoma. Human Hiphum 222 was found to be primarily expressed
 CC in testes, trachea and lung, cerebellum and adipose tissue. When Taqman
 CC was carried out on a respiratory disease plate, Hiphum 222 was also found
 CC to be expressed in samples from lungs of chronic obstructive pulmonary
 CC disease (COPD) and asthma patients. The chromosomal localization of human
 CC Hiphum 222 was mapped to chromosome 11p15.4.

SQ Sequence 575 AA;

Query Match 100.0%; Score 2989; DB 7; Length 575;

Best Local Similarity 100.0%; Pred. No. 8.7e-278; Mismatches 0; Indels 0; Gaps 0;

Matches 575; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQDTRKVTETSSPPAPSPAPSKARLLPVLPSGDYYTWMNTWVPVWYLLIIVCRACFPD 60
 DB 1 MSQDTRKVTETSSPPAPSPAPSKARLLPVLPSGDYYTWMNTWVPVWYLLIIVCRACFPD 60
 QY 61 LQHGVLVAMLVLDYSDLLYLDDMVVRFATGFLGEGILVVDGRISSRYVRTWSPFLDLA 120
 DB 61 LQHGVLVAMLVLDYSDLLYLDDMVVRFATGFLGEGILVVDGRISSRYVRTWSPFLDLA 120
 QY 121 SLMPFDVVVYVRGPTPTLRLNRLRAPLRFAPRTERTEYTPAFAFRJAKMLYFVVI 180
 DB 121 SLMPFDVVVYVRGPTPTLRLNRLRAPLRFAPRTERTEYTPAFAFRJAKMLYFVVI 180
 QY 181 HNSNCLFYALSLRYLFGGRDAWVYPPDAPGFERLRQYLYSEYFSTLIITVGDTPPPAR 240
 DB 181 HNSNCLFYALSLRYLFGGRDAWVYPPDAPGFERLRQYLYSEYFSTLIITVGDTPPPAR 240
 QY 241 EEEYLFPMGDELLAWGFAITNGSMSSVYNNNTADAAPYPPHALYKTKMKIQHVRKLE 300
 DB 241 EEEYLFPMGDELLAWGFAITNGSMSSVYNNNTADAAPYPPHALYKTKMKIQHVRKLE 300
 QY 301 RRVIDMYGHLQINKKMTNEVALIQHLPETLRABAVNSVHLSTLSRVQIFONCEASLLEEL 360
 DB 301 RRVIDMYGHLQINKKMTNEVALIQHLPETLRABAVNSVHLSTLSRVQIFONCEASLLEEL 360
 QY 361 VLKIQPQYVSPGEYVCRKGDIGQEMYIIRREGQLAVVADDTQYAVLGAAGLYFGESIIIN 420
 DB 361 VLKIQPQYVSPGEYVCRKGDIGQEMYIIRREGQLAVVADDTQYAVLGAAGLYFGESIIIN 420
 QY 421 IKGNSGNRRNTANISLGSIDFLCLSKEDLREVLSEYPAQITIMEKREILLKNNKLDV 480

DB 421 IKGNSGNRRNTANISLGSIDFLCLSKEDLREVLSEYPAQITIMEKREILLKNNKLDV 480
 QY 481 NABAERIALQATSRRLGDLQDDLDQTKFARLLAELESSALKIAYRIERLEWOTREMP 540
 DB 481 NABAERIALQATSRRLGDLQDDLDQTKFARLLAELESSALKIAYRIERLEWOTREMP 540
 QY 541 MPEDLAEDDEGEPEEGTSKDEGRASQEGPPGPE 575
 DB 541 MPEDLAEDDEGEPEEGTSKDEGRASQEGPPGPE 575

RESULT 7

AA014138 standard; protein; 575 AA.

AA014138;

01-MAY-2002 (first entry)

Human transporter and ion channel (TRICH-1) protein.

KW Human; transporter and ion channel protein; TRICH-1;
 KW cell electrical potential; screening; transport disorder;
 KW Parkinson's disease; diabetes mellitus; neurological disorder;
 KW Alzheimer's disease; amnesia; Parkinson's disease; multiple sclerosis;
 KW cell proliferative disorder; cancer; leukaemia; immunological disorder;
 KW AIDS; asthma; muscle disorder; migraine; hypertension.

Homo sapiens.

WO200202633-A2.

10-JAN-2002.

27-JUN-2001; 2001WO-US020702.

29-JUN-2000; 2000US-0215391P.

(INCY-) INCYTE GENOMICS INC.

Raumann BE, Sanjanwala MS, Tribouley CM, Walla NK;

WPI; 2002-148001/19.

N-PSDB; AAL41869.

PT Novel isolated human transporter and ion channel (TRICH-1) polypeptide,
 PT useful for treating and preventing transport disorders e.g. ataxia
 PT telangiectasia, diabetes mellitus, myasthenia gravis, diabetes insipidus.
 PS Claim 1; Page 104-105; 106pp; English.

CC The present sequence represents the human transporter and ion channel
 CC (TRICH-1) protein of the invention. The electrical potential of a cell is
 CC generated and maintained by controlling the movement of ions across the
 CC plasma membrane. The movement of ions requires ion channels, of which
 CC there are two types: ion transporters and gated ion channels. The
 CC invention comprises the the nucleotide and protein sequences of TRICH-1.
 CC The TRICH-1 nucleotide and protein sequences are useful for screening
 CC compounds as agonists or antagonists of TRICH-1. The TRICH-1 nucleotide
 CC and protein are also useful in the diagnosis, treatment and prevention
 CC of: transport disorders (e.g. Parkinson's disease and diabetes mellitus);
 CC neurological disorders associated with transport (e.g. Alzheimer's
 CC disease and amnesia); neurological disorders (e.g. Parkinson's disease
 CC and multiple sclerosis); cell proliferative disorders (e.g. cancer and
 CC leukaemia); immunological disorders (e.g. AIDS and asthma); and muscle
 CC disorders (e.g. migraine and hypertension). The TRICH-1 nucleotide may
 CC also be used for generating hybridisation probes to map the naturally
 CC occurring TRICH-1 genomic sequences and detecting differences in
 CC chromosomal location

SQ Sequence 575 AA;

Query Match 99.8%; Score 2984; DB 5; Length 575;

Best Local Similarity 99.8%; Pred. No. 2.6e-277;
Matches 574; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MSODTRKVTETSSPPAPSKARLLPVLDSGGDYVYWMNTMVPVWYNLIILVCRACFPD 60
DB 1 MSODTRKVTETSSPPAPSKARLLPVLDSGGDYVYWMNTMVPVWYNLIILVCRACFPD 60
QY 61 LQHGVLVAMLVVDYSDLLYLDMVVRFTGTGLEOGILVVDKGRISRRVYRTWSPFLDLA 120
DB 61 LQHGVLVAMLVVDYSDLLYLDMVVRFTGTGLEOGILVVDKGRISRRVYRTWSPFLDLA 120
QY 121 SLMPDVVVYVRLGPHPTLRLNRLFLAPRLFEAFDRTETRTAYPNAFRJAKMLYIFVVI 180
DB 121 SLMPDVVVYVRLGPHPTLRLNRLFLAPRLFEAFDRTETRTAYPNAFRJAKMLYIFVVI 180
QY 181 HNNSCLYFALSRYLGGRDAMVYPPDPAQGFERLRQYLYSYFSTLITTTGDPDPPAR 240
DB 181 HNNSCLYFALSRYLGGRDAMVYPPDPAQGFERLRQYLYSYFSTLITTTGDPDPPAR 240
QY 241 EEEYLFMVGDFLAVWGFAITGMSMSVLYNNMTADAIFYPDHALVKKYMKLQHVNRKLE 300
DB 241 EEEYLFMVGDFLAVWGFAITGMSMSVLYNNMTADAIFYPDHALVKKYMKLQHVNRKLE 300
QY 301 RRVIDMYQHLQINKKNTNEVALLOHLPERLRABAVAVSVHLSLRSVQIFONCEASLLEEL 360
DB 301 RRVIDMYQHLQINKKNTNEVALLOHLPERLRABAVAVSVHLSLRSVQIFONCEASLLEEL 360
QY 361 VLKLPQRTYSPGEYCRKDKDIGOEMTIREGQLAVVADGCIQYAVLAGLYFGEISIN 420
DB 361 VLKLPQRTYSPGEYCRKDKDIGOEMTIREGQLAVVADGCIQYAVLAGLYFGEISIN 420
QY 421 IKGNSGNRRTANIKSLGYSDLFCLSKEDREVLSEYPOAQTMEKREIILKKMKLV 480
DB 421 IKGNSGNRRTANIKSLGYSDLFCLSKEDREVLSEYPOAQTMEKREIILKKMKLV 480
QY 481 NAEAAEIALQEAATESRLRGDQDLQTKFARLLAELESSALKIAYRIERLEWQTRWP 540
DB 481 NAEAAEIALQEAATESRLRGDQDLQTKFARLLAELESSALKIAYRIERLEWQTRWP 540
QY 541 MPEDLAEDDBEGPEEGTSGKDEBGRASQSGPPGE 575
DB 541 MPEDLAEDDBEGPEEGTSGKDEBGRASQSGPPGE 575

RESULT 8
AAM47673
ID AAM47673 standard; protein; 575 AA.
AC AAM47673;
XX
XX 21-FEB-2002 (first entry)
XX
XX DE MOL10b protein sequence.
XX
XX KM MOL; G-coupled protein-receptor; cardiomyopathy; atherosclerosis;
XX KM cell signal processing; metabolic disorder; diabetes; cancer; human;
XX KM neurodegenerative disorder; immune disorder; cardiac disorder;
XX KM lung disease; autoimmune disease; developmental disorder; antidiabetic;
XX KM Cystostatic; Neuroprotective; Antiatherosclerotic; Immunosuppressive;
XX KM Gene therapy; Vaccine; antiinflammatory; MOL10b.
XX
XX OS Homo sapiens.
XX
XX PN WO200181578-A2.
XX
XX PD 01-NOV-2001.
XX
XX PF 26-APR-2001; 2001WO-US013578.
XX
XX PR 26-APR-2000; 2000US-0200158P.
XX PR 28-APR-2000; 2000US-0200613P.
XX PR 28-APR-2000; 2000US-0200780P.
XX PR 01-MAY-2000; 2000US-0201006P.

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PR 01-MAY-2000; 2000US-0201007P.
PR 01-MAY-2000; 2000US-0201236P.
PR 01-MAY-2000; 2000US-0201238P.
PR 02-MAY-2000; 2000US-0201186P.
PR 03-MAY-2000; 2000US-0201474P.
PR 03-MAY-2000; 2000US-0201508P.
PR 25-JUL-2000; 2000US-0220591P.
PR 15-SEP-2000; 2000US-0232678P.
PR 22-JAN-2001; 2001US-0263217P.
PR 30-JAN-2001; 2001US-0265160P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Vernet CAM, Fernandes ER, Gerlach V, Shinkens RA, Maljankar UM;
XX Bollog FL, Zehusen BD, Spytek KA, Majumder K, Tchernev VT;
XX Padigan M, Paturajan M, Burgess CB, Gangoli EA, Sathson G;
XX Rastelli L, Macdougall JR, Taupier RJ, Grosse WM, Szekeres ES;
XX Alsbrook JP;
XX
XX WPI: 2002-049278/06.
XX N-PSDB; ABA04603.
XX
XX Novel G-protein coupled receptor-related polypeptides and polynucleotides
XX for diagnosing, preventing and treating cardiomyopathy, atherosclerosis,
XX disorders related to cell signal processing and for identifying
XX modulators.
XX
XX Claim 1; Page 79; 227pp; English.
XX
XX The present invention relates to novel G-coupled protein-receptor related
XX proteins and coding sequences (MOLX, where X is a number from 1 to 10,
XX ABA04589-ABA04603 and AAM47659-AAM47673). MOLX proteins and coding
XX sequences are useful for treating or preventing a MOLX-associated
XX disorder, such as cardiomyopathy, atherosclerosis, disorders related to
XX cell signal processing and metabolic pathway modulation, diabetes and
XX cancer. Additionally, MOLX proteins and coding sequences are useful for
XX preventing and treating a variety of disorders including metabolic
XX disorders, nutritional oedema, chronic and hereditary pancreaticitis,
XX obesity, infectious disease, anorexia, neurodegenerative disorders,
XX Alzheimer's disease, Parkinson's disease, stroke, immune disorders,
XX haematopoietic disorders and various dyslipidaemias, metabolic syndrome X
XX and wasting disorders associated with chronic diseases and cancers,
XX cardiac disorders, hypertension, hypercalcaemia, cirrhosis, angiodeniasis,
XX and wound healing, trauma, glomerulonephritis, hyper and hypothyroidism,
XX multiple sclerosis, lung diseases including asthma, Crohn's disease,
XX scleroderma, autoimmune diseases, developmental disorders and neural tube
XX defects. The present sequence is the protein sequence for human MOL10b.
XX CC MOL10b protein is a cyclic nucleotide-gated olfactory channel-like
XX protein
XX
XX SO Sequence 575 AA;
XX
XX Query Match 99.8%; Score 2984; DB 5; Length 575;
XX Best Local Similarity 99.8%; Pred. No. 2.6e-277;
XX Matches 574; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MSODTRKVTETSSPPAPSKARLLPVLDSGGDYVYWMNTMVPVWYNLIILVCRACFPD 60
DB 1 MSODTRKVTETSSPPAPSKARLLPVLDSGGDYVYWMNTMVPVWYNLIILVCRACFPD 60
QY 61 LQHGVLVAMLVVDYSDLLYLDMVVRFTGTGLEOGILVVDKGRISRRVYRTWSPFLDLA 120
DB 61 LQHGVLVAMLVVDYSDLLYLDMVVRFTGTGLEOGILVVDKGRISRRVYRTWSPFLDLA 120
QY 121 SLMPDVVVYVRLGPHPTLRLNRLFLAPRLFEAFDRTETRTAYPNAFRJAKMLYIFVVI 180
DB 121 SLMPDVVVYVRLGPHPTLRLNRLFLAPRLFEAFDRTETRTAYPNAFRJAKMLYIFVVI 180
QY 181 HNNSCLYFALSRYLGGRDAMVYPPDPAQGFERLRQYLYSYFSTLITTTGDPDPPAR 240
DB 181 HNNSCLYFALSRYLGGRDAMVYPPDPAQGFERLRQYLYSYFSTLITTTGDPDPPAR 240
QY 241 EEEYLFMVGDFLAVWGFAITGMSMSVLYNNMTADAIFYPDHALVKKYMKLQHVNRKLE 300

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DB      ||| 241 EEEYLFMWGDFLLAWGFAITGSMSSVYNNMTADAAFYDPHALVKKYMKLQHNKKE 300
QY      ||| 301 RRVIMVYQHLOINKKMTNEVALIQLHPELRRAEVAVSVAHLSLTSRVOIFONCEASLLEEL 360
DB      ||| 301 RRVIMVYQHLOINKKMTNEVALIQLHPELRRAEVAVSVAHLSLTSRVOIFONCEASLLEEL 360
QY      ||| 361 VKLQPOPTYSPEEYVCRKGDIGQEMYYIIRREGQLAVVADGGITQYAVLGAAGLYFGEISLIN 420
DB      ||| 361 VKLQPOPTYSPEEYVCRKGDIGQEMYYIIRREGQLAVVADGGITQYAVLGAAGLYFGEISLIN 420
QY      ||| 421 IKGNSGNRRNTANIKSLGYSDLFCLSKEDLREVLSEYPOAQTIMEKREILLKNNKLDV 480
DB      ||| 421 IKGNSGNRRNTANIKSLGYSDLFCLSKEDLREVLSEYPOAQTIMEKREILLKNNKLDV 480
QY      ||| 481 NAEAEIALQEAATESRLRGIDQDLDTQTKFARLLAELESSALKIAYRIERLEWQTRWP 540
DB      ||| 481 NAEAEIALQEAATESRLRGIDQDLDTQTKFARLLAELESSALKIAYRIERLEWQTRWP 540
QY      ||| 541 MPEDLAADDEGEPEEGTSKDEGRASQEGPPE 575
DB      ||| 541 MPEDLAADDEGEPEEGTSKDEGRASQEGPPE 575

RESULT 9
ADJ87678 standard; protein; 575 AA.
AC      ADJ87678;
DT      06-MAY-2004 (first entry)
XX      G-coupled protein receptor-related protein #15.
DE      G-coupled protein receptor-related protein #15.
XX      novel protein; G-coupled protein receptor-related protein;
XX      cardiomyopathy; atherosclerosis; cell signal processing-related disorder;
XX      metabolic pathway modulation-related disorder; diabetes; cancer; stroke;
XX      Huntington's disease; epilepsy; anxiety; pain; hypercholesterolaemia;
XX      obesity; hypertension; Crohn's disease; systemic lupus erythematosus;
XX      viral infections; bacterial infection; parasitic infection;
XX      hyperthyroidism; hypothyroidism; Von Hippel-Lindau syndrome;
XX      Alzheimer's disease; tuberous sclerosis; hypercalcaemia; cerebral palsy.
XX      Unidentified.
XX      MO2002102321-AA2.
PN      27-DEC-2002.
PD      18-JUN-2002; 2002MO-US019522.
PF      18-JUN-2001; 2001US-0298994P.
PR      18-JUN-2001; 2001US-0298994P.
PR      04-OCT-2001; 2001US-00972446.
PR      06-JUN-2002; 2002US-00299134.
PR      07-JUN-2002; 2002US-00298994.
PA      (CURA-) CURAGEN CORP.
XX      Anderson DW, Guo X, Gusev VY, Herrmann JL, Li L, Mezes PS;
PI      Pena CEA, Spaderna SK, Zhong M;
XX      WPI; 2003-167441/16.
DR      N-PSDB; ADJ87677.
XX      New MOLX polypeptides and polymucleotides, useful in gene therapy,
XX      particularly for treating or preventing e.g. cardiomyopathy,
XX      atherosclerosis, diabetes, adenoma, brain tumor, breast cancer, prostate
XX      cancer, stroke or pain.
XX      Claim 1; SEQ ID NO 30; 378bp; English.
XX      The invention comprises the amino acid and coding sequences of novel G-

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CC      coupled protein receptor-related (MOL) proteins. The DNA and protein
CC      sequences of the invention are useful for treating or preventing a MOL-
CC      associated disorder, such as: cardiomyopathy, atherosclerosis, disorders
CC      associated with cell signal processing and metabolic pathway modulation,
CC      or diabetes. The DNA and protein sequences are also useful for the
CC      treatment of: cancer, stroke, Huntington's disease, epilepsy, anxiety,
CC      pain, hypercholesterolaemia, obesity, hypertension, Crohn's disease,
CC      systemic lupus erythematosus, viral infections, bacterial infections,
CC      parasitic infections, hyperthyroidism, hypothyroidism, Von Hippel-Lindau
CC      syndrome, Alzheimer's disease, tuberous sclerosis, hypercalcaemia, or
CC      cerebral palsy. The present amino acid sequence represents a MOL protein
CC      of the invention.
SQ      Sequence 575 AA;
QY      Query Match 99.8%; Score 2984; DB 7; Length 575;
DB      Best Local Similarity 99.8%; Pred. No. 2.6e-27;
DB      Matches 574; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      1 MSODTKYKTTSSPPAPSKARKLLPVLDPGSDYYWMLNTMPPVMTNLIIVCRACFPD 60
DB      1 MSODTKYKTTSSPPAPSKARKLLPVLDPGSDYYWMLNTMPPVMTNLIIVCRACFPD 60
QY      61 LQHGTYAMLVLDYTSLLYLDMVVRFTGFLQGLIYVVDKGRISRYVTSFPLDLA 120
DB      61 LQHGTYAMLVLDYTSLLYLDMVVRFTGFLQGLIYVVDKGRISRYVTSFPLDLA 120
QY      121 SLMPDVVYVRLGPHPTTLRLNRLRAPRLFEAFDRTEFTRAVFNARIAKMLYIFVVI 180
DB      121 SLMPDVVYVRLGPHPTTLRLNRLRAPRLFEAFDRTEFTRAVFNARIAKMLYIFVVI 180
QY      181 HMNSCLYPALSRVYGFGRDAWVYDDPAQPGFERLRROYLYSFYSTLILTTVGTPPPAR 240
DB      181 HMNSCLYPALSRVYGFGRDAWVYDDPAQPGFERLRROYLYSFYSTLILTTVGTPPPAR 240
QY      241 EEEYLFMWGDFLLAWGFAITGSMSSVYNNMTADAAFYDPHALVKKYMKLQHNKKE 300
DB      241 EEEYLFMWGDFLLAWGFAITGSMSSVYNNMTADAAFYDPHALVKKYMKLQHNKKE 300
QY      301 RRVIMVYQHLOINKKMTNEVALIQLHPELRRAEVAVSVAHLSLTSRVOIFONCEASLLEEL 360
DB      301 RRVIMVYQHLOINKKMTNEVALIQLHPELRRAEVAVSVAHLSLTSRVOIFONCEASLLEEL 360
QY      361 VKLQPOPTYSPEEYVCRKGDIGQEMYYIIRREGQLAVVADGGITQYAVLGAAGLYFGEISLIN 420
DB      361 VKLQPOPTYSPEEYVCRKGDIGQEMYYIIRREGQLAVVADGGITQYAVLGAAGLYFGEISLIN 420
QY      421 IKGNSGNRRNTANIKSLGYSDLFCLSKEDLREVLSEYPOAQTIMEKREILLKNNKLDV 480
DB      421 IKGNSGNRRNTANIKSLGYSDLFCLSKEDLREVLSEYPOAQTIMEKREILLKNNKLDV 480
QY      481 NAEAEIALQEAATESRLRGIDQDLDTQTKFARLLAELESSALKIAYRIERLEWQTRWP 540
DB      481 NAEAEIALQEAATESRLRGIDQDLDTQTKFARLLAELESSALKIAYRIERLEWQTRWP 540
QY      541 MPEDLAADDEGEPEEGTSKDEGRASQEGPPE 575
DB      541 MPEDLAADDEGEPEEGTSKDEGRASQEGPPE 575

RESULT 10
ABU09778 standard; protein; 575 AA.
ID      ABU09778
XX      ABU09778;
AC      05-AUG-2003 (first entry)
XX      Human transporter variant polypeptide.
XX      Human; transporter.
XX      Homo sapiens.
OS

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XX Key Location/Qualifiers
FH Misc-difference 317
FT /note= "Encoded by TCC"
FT Misc-difference 432
FT /note= "Encoded by ACC"
FT Misc-difference 476
FT /note= "Encoded by AGC"
FT Misc-difference 553
FT /note= "Glu substituted by Val"
PN US2003013156-A1.
PD 16-JAN-2003.
XX
XX 31-JUL-2002; 2002US-00207951.
XX
XX 13-JUN-2000; 2000US-0211223F.
XX 14-DEC-2000; 2000US-00735932.
XX
XX (APPL-) APPLERA CORP.
XX
XX Guejler K, Ketchum KA, Di Francesco V, Beasley EM;
PI WPI; 2003-416799/39.
DR
XX New transporter proteins related to cyclic nucleotide-gated ion channel
PT subfamily and polynucleotide encoding the protein for diagnosing,
PT treating diseases mediated by transporter protein and identifying
PT modulators.
XX
XX Disclosure; Page: 52pp; English.
XX
XX The invention relates to an isolated human transporter polypeptide and
CC the polynucleotide encoding it. The polypeptide is useful for identifying
CC a modulator of the expression of the protein by contacting the protein
CC with an agent and determining if the agent has modulated the function,
CC activity or expression of the protein. The agent is administered to a
CC host cell comprising an expression vector that expresses the protein. The
CC polypeptide is also useful for identifying an agent that binds to the
CC polypeptide and for treating a disease or condition mediated by a human
CC transporter protein. The polypeptide and polynucleotide are useful as
CC models for the development of human therapeutic targets, to aid in the
CC identification of therapeutic proteins and to serve as targets for the
CC development of human therapeutic agents that modulate transporter
CC activity in cells and tissues that express the transporter. The
CC polypeptide is useful for raising antibodies or for eliciting another
CC immune response, as a reagent in assays designed to quantitatively
CC determine levels of the protein in biological fluids, as markers for
CC tissues in which the corresponding protein is expressed and to identify
CC the binding partner/ligand so as to develop a system to identify
CC inhibitors of the binding interactions. This sequence represents a human
CC transporter variant polypeptide of the invention. Note: This sequence is
CC not featured in the specification but was derived from the polypeptide
CC shown in ABU09091
XX
XX Sequence 575 AA;
SQ
Query Match 99.8%; Score 2982; DB 6; Length 575;
Best Local Similarity 99.8%; Pred. No. 4.1e-277;
Matches 574; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MSQDTRKVTSSPPSPKARKLLPVLDSGGYYWMLTMMFPVWYNLIIVCRACFPD 60
DB 1 MSQDTRKVTSSPPSPKARKLLPVLDSGGYYWMLTMMFPVWYNLIIVCRACFPD 60
QY 61 LQHGVLAVMLVDYTSDDLVLDDMVVRFHTGFLQGLIIVDKGRISRRVYRTWSFPLDA 120
DB 61 LQHGVLAVMLVDYTSDDLVLDDMVVRFHTGFLQGLIIVDKGRISRRVYRTWSFPLDA 120
QY 121 SIMPTDVVYVRLGPHPTPLRLNRFAPRLFEAFDTRTETRTAVPNAFRIAKMLYIFVYI 180
DB 121 SIMPTDVVYVRLGPHPTPLRLNRFAPRLFEAFDTRTETRTAVPNAFRIAKMLYIFVYI 180
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QY 181 HNSCLYFALSRYLGFGRDAMVYPPAPQGFERLRLROYLYSFSTLILTTVGTTPPPAR 240
DB 181 HNSCLYFALSRYLGFGRDAMVYPPAPQGFERLRLROYLYSFSTLILTTVGTTPPPAR 240
QY 241 EEEYLFVWGDFLLAVMGFATIMGSSSVIYNNNTDAAFPYPDHALVKKYMKLQHVNRKLE 300
DB 241 EEEYLFVWGDFLLAVMGFATIMGSSSVIYNNNTDAAFPYPDHALVKKYMKLQHVNRKLE 300
QY 301 RRVIDWYHLOINRKTMEVAILQHLPERLRAEVSVHLSLTSVQIFQNCESLLEBL 360
DB 301 RRVIDWYHLOINRKTMEVAILQHLPERLRAEVSVHLSLTSVQIFQNCESLLEBL 360
QY 361 VLKLPQTYSPGEYVCRKADIGQEMYYIIREGLAVVADGITQYAVLAGYFGEISLIN 420
DB 361 VLKLPQTYSPGEYVCRKADIGQEMYYIIREGLAVVADGITQYAVLAGYFGEISLIN 420
QY 421 IKGNMSGNRRRTANIKSLGYSDLFCLSKEDLREVLSEYFQAQTIMBEKREIILKNKLDV 480
DB 421 IKGNMSGNRRRTANIKSLGYSDLFCLSKEDLREVLSEYFQAQTIMBEKREIILKNKLDV 480
QY 481 NAEAEIALQENTESRLGLDQQLDLOTKPARLLAELESSALKIAYRIERLEMTREMP 540
DB 481 NAEAEIALQENTESRLGLDQQLDLOTKPARLLAELESSALKIAYRIERLEMTREMP 540
QY 541 MPEDLAEDDEGEVPEEGTSKDEGRASQEGPPGPE 575
DB 541 MPEDLAEDDEGEVPEEGTSKDEGRASQEGPPGPE 575
RESULT 11
AAM47672
ID AAM47672 standard; protein; 578 AA.
XX
XX AAM47672;
XX
XX 21-FEB-2002 (first entry)
XX
XX MOL10a protein sequence.
XX
XX MOL1; G-coupled protein-receptor; cardiomyopathy; atherosclerosis;
KW cell signal processing; metabolic disorder; diabetes; cancer;
KW neurodegenerative disorder; immune disorder; cardiac disorder;
KW lung disease; autoimmune disease; developmental disorder; anti-diabetic;
KW Cytostatic; Neuroprotective; Antiatherosclerotic; Immunosuppressive;
KW Gene therapy; Vaccine; antiinflammatory; MOL10a.
XX
XX Unidentified.
OS
XX
XX MO200181578-A2.
PN
XX
XX 01-NOV-2001.
XX
XX 26-APR-2001; 2001WO-US013578.
XX
XX 26-APR-2000; 2000US-0200158P.
PR 26-APR-2000; 2000US-0200613P.
PR 28-APR-2000; 2000US-0200780P.
PR 01-MAY-2000; 2000US-0201006P.
PR 01-MAY-2000; 2000US-0201007P.
PR 01-MAY-2000; 2000US-0201236P.
PR 01-MAY-2000; 2000US-0201238P.
PR 02-MAY-2000; 2000US-0201186P.
PR 03-MAY-2000; 2000US-0201474P.
PR 03-MAY-2000; 2000US-0201508P.
PR 25-JUL-2000; 2000US-0220591P.
PR 15-SEP-2000; 2000US-0232678P.
PR 22-JAN-2001; 2001US-0263217P.
PR 30-JAN-2001; 2001US-0265160P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Vernet CAM, Fernandes ER, Gerlach V, Shinkets RA, Maljankar UM;
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PI Bol'dog FL, Zernusen BD, Spytek KA, Majumder K, Tchernev VT;
 PI Padigaru M, Paturajan M, Burgess CE, Gangolli EA, Smithson G;
 PI Rastelli L, Macdougall JR, Taupier RJ, Grosse WM, Szekeres ES;
 PI Alsebrook JP;
 XX
 DR WPI: 2002-049278/06.
 DR N-PSDB; ABA04602.

PT Novel G-protein coupled receptor-related polypeptides and polynucleotides
 PT for diagnosing, preventing and treating cardiomyopathy, atherosclerosis,
 PT disorders related to cell signal processing and for identifying
 PT modulators.

XX
 PS Claim 1; Page 77; 227pp; English.

CC The present invention relates to novel G-coupled protein-receptor related
 CC proteins and coding sequences (MOLX, where X is a number from 1 to 10,
 CC ABA04589-ABA04603 and AAM47659-AAM47673). MOLX proteins and coding
 CC sequences are useful for treating or preventing a MOLX-associated
 CC disorder, such as cardiomyopathy, atherosclerosis, disorders related to
 CC cell signal processing and metabolic pathway modulation, diabetes and
 CC cancer. Additionally, MOLX proteins and coding sequences are useful for
 CC preventing and treating a variety of disorders including metabolic
 CC disorders, nutritional oedema, chronic and hereditary pancreatitis,
 CC obesity, infectious disease, anorexia, neurodegenerative disorders,
 CC Alzheimer's disease, Parkinson's disease, stroke, immune disorders,
 CC haematopoietic disorders and various dyslipidaemias, metabolic syndrome X
 CC and wasting disorders associated with chronic diseases and cancers,
 CC cardiac disorders, hypertension, hypercalcaemia, cirrhosis, angiodysplasia
 CC and wound healing, trauma, glomerulonephritis, hyper and hypothyroidism,
 CC multiple sclerosis, lung diseases including asthma, Crohn's disease,
 CC scleroderma, autoimmune diseases, developmental disorders and neural tube
 CC defects. The present sequence is the protein sequence for MOL10a. MOL10a
 CC protein is a cyclic nucleotide-gated olfactory channel-like protein
 XX
 XX Sequence 578 AA;

Query Match 98.9%; Score 2957.5; DB 5; Length 578;
 Best Local Similarity 99.5%; Pred. No. 9.4e-275;
 Matches 575; Conservative 0; Mismatches 0; Indels 3; Gaps 3;

QY 1 MSQDTRKVTETSSPPAPSKA-RKLPLVLDPSGDYVYMMNTMVFPMVNLIIIVCRACP 59
 DB 1 MSQDTRKVTETSSPPAPSKARKLLPVLDPSCDYVYMMNTMVFPMVNLIIIVCRACP 60
 QY 60 DLQHGIVLAVMLVLDYTSLLYLIDMVVRHPT-GELEGILVVDKGRISRRYRWSPFLD 118
 DB 61 DLQHGIVLAVMLVLDYTSLLYLIDMVVRHPTGEGLEGILVVDKGRISRRYRWSPFLD 120
 QY 119 LASLMPDVVVYRLGPHPTLRLNRFAPRLFAFPDTERTRAYPNAFRATKMLYIFV 178
 DB 121 LASLMPDVVVYRLGPHPTLRLNRFAPRLFAFPDTERTRAYPNAFRATKMLYIFV 180
 QY 179 VIHNSCIYFALSRYLFGRDAMVYPDAPGFERLRQVLYSFFSTLLITVGDTPPP 238
 DB 181 VIHNSCIYFALSRYLFGRDAMVYPDAPGFERLRQVLYSFFSTLLITVGDTPPP 240
 QY 239 ARESEYLFMVGDFLLAVGFAFMGSSSVYVNTADAAVPPHAIYKMKQOVNRK 298
 DB 241 ARESEYLFMVGDFLLAVGFAFMGSSSVYVNTADAAVPPHAIYKMKQOVNRK 300
 QY 299 LERRIVIMYQHLQINKKTNVEALLOHLPERLRAEVAVSYLSTLSVOJFONCEASLLE 358
 DB 301 LERRIVIMYQHLQINKKTNVEALLOHLPERLRAEVAVSYLSTLSVOJFONCEASLLE 360
 QY 359 ELVVLKLOPQYSSREYVCRKDDIQEYIIRREGOLAVVADGITYAVLAGLYFGESL 418
 DB 361 ELVVLKLOPQYSSREYVCRKDDIQEYIIRREGOLAVVADGITYAVLAGLYFGESL 420
 QY 419 INIK-GMNSGNRRRANIKSLGYSDLPCLSKEDLREVLSEVPOQOTTMEEGRETIILKMK 477
 DB 421 INIK-GMNSGNRRRANIKSLGYSDLPCLSKEDLREVLSEVPOQOTTMEEGRETIILKMK 480

QY 478 LVNABAEIALVQETESRLRGDLDDLOTFARLLAEISSALKIAYRIERLEWQTR 537
 DB 481 LVNABAEIALVQETESRLRGDLDDLOTFARLLAEISSALKIAYRIERLEWQTR 540
 QY 538 EWPMPEDLAEADDEPEEGTSKDEGRASQSGPPGPE 575
 DB 541 EWPMPEDLAEADDEPEEGTSKDEGRASQSGPPGPE 578

RESULT 12
 ADJ87676
 ID ADJ87676 standard; protein; 578 AA.
 XX
 AC ADJ87676;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE G-coupled protein receptor-related protein #14.

XX novel protein; G-coupled protein receptor-related protein;
 KW cardiomyopathy; atherosclerosis; cell signal processing-related disorder;
 KW metabolic pathway modulation-related disorder; diabetes; cancer; stroke;
 KW Huntington's disease; epilepsy; anxiety; pain; hypercholesterolaemia;
 KW obesity; hypertension; Crohn's disease; systemic lupus erythematosus;
 KW viral infections; bacterial infection; parasitic infection;
 KW hyperthyroidism; hypothyroidism; Von Hippel-Lindau syndrome;
 KW Alzheimer's disease; tuberculous sclerosis; hypercalcaemia; cerebral palsy.
 OS Unidentified.
 XX
 PN WO2002102321-A2.
 XX
 PD 27-DEC-2002.
 XX
 PF 18-JUN-2002; 2002WO-05019522.
 XX
 PR 18-JUN-2001; 2001US-0298994P.
 PR 18-JUN-2001; 2001US-0299134P.
 PR 04-OCT-2001; 2001US-00972446.
 PR 06-JUN-2002; 2002US-00299134.
 PR 07-JUN-2002; 2002US-00298994.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Anderson DW, Guo X, Gusev VY, Herrmann JL, Li L, Mezes PS;
 PI Pena CEA, Spaderna SK, Zhong M;
 XX
 DR WPI: 2003-167441/16.
 XX
 DR N-PSDB; ADJ87675.

XX New MOLX polypeptides and polynucleotides, useful in gene therapy,
 PT particularly for treating or preventing e.g. cardiomyopathy,
 PT atherosclerosis, diabetes, adenoma, brain tumor, breast cancer, prostate
 PT cancer, stroke or pain.
 XX
 PS Claim 1; SEQ ID NO 28; 378pp; English.

XX The invention comprises the amino acid and coding sequences of novel G-
 CC coupled protein receptor-related (MOL) proteins. The DNA and protein
 CC sequences of the invention are useful for treating or preventing a MOL-
 CC associated disorder, such as: cardiomyopathy, atherosclerosis, disorders
 CC associated with cell signal processing and metabolic pathway modulation,
 CC or diabetes. The DNA and protein sequences are also useful for the
 CC treatment of: cancer, stroke, Huntington's disease, epilepsy, anxiety,
 CC pain, hypercholesterolaemia, obesity, hypertension, Crohn's disease,
 CC systemic lupus erythematosus, viral infections, bacterial infections,
 CC parasitic infections, hyperthyroidism, hypothyroidism, Von Hippel-Lindau
 CC syndrome, Alzheimer's disease, tuberculous sclerosis, hypercalcaemia, or
 CC cerebral palsy. The present amino acid sequence represents a MOL protein
 CC of the invention.

XX Sequence 578 AA;

Query Match 98.9%; Score 2957.5; DB 7; Length 578;
 Best Local Similarity 99.5%; Pred. No. 9.4e-275;
 Matches 575; Conservative 0; Mismatches 0; Indels 3; Gaps 3;

QY 1 MSQDTKVTETSSPPAPSKA-RKLLPVLDPGSDYYMMNTMVPFVMTNLLVCRACP 59
 DB 1 MSQDTKVTETSSPPAPSKARKLLPVLDPGSDYYMMNTMVPFVMTNLLVCRACP 60
 QY 60 DLQHGVLVAVLVDTSLLYLDMVVRPHT-GELEGGLVVDKGRISRRYRTSFLD 118
 DB 61 DLQHGVLVAVLVDTSLLYLDMVVRPHTGFLGGLVVDKGRISRRYRTSFLD 120
 QY 119 LASLMPDVVYVRLGPHPTLRLNRLPRLPFLFAFDRTETRTAYPNARLAKLMLYFV 178
 DB 121 LASLMPDVVYVRLGPHPTLRLNRLPRLPFLFAFDRTETRTAYPNARLAKLMLYFV 180
 QY 179 VIHNSCLYFALSRYLFGRDAMVY PDPAPQGFEBRLRQYLYSPFSTLLITVGDTPPP 238
 DB 181 VIHNSCLYFALSRYLFGRDAMVY PDPAPQGFEBRLRQYLYSPFSTLLITVGDTPPP 240
 QY 229 AREEYILFMVGDFLAAMVGFATIMSGSSVYINMTADAAFPBDALVKKYKMLQHVNRK 298
 DB 241 AREEYILFMVGDFLAAMVGFATIMSGSSVYINMTADAAFPBDALVKKYKMLQHVNRK 300
 QY 299 LERRVYIDWYQHLQINKKMTNEVALIQHLPERLRAEVAVSVHSTLSRVQIFONCEASLLE 358
 DB 301 LERRVYIDWYQHLQINKKMTNEVALIQHLPERLRAEVAVSVHSTLSRVQIFONCEASLLE 360
 QY 359 ELVLKLPQYTSFGYVCRKGDIGQEMTIIREGQLAVVADGDIITYAVLAGLYFGEISI 418
 DB 361 ELVLKLPQYTSFGYVCRKGDIGQEMTIIREGQLAVVADGDIITYAVLAGLYFGEISI 420
 QY 419 INIK-GNMSGNRTANIKSLGSDIFCLSKEDLREVLSEYPAQITMEKKEIILLKMK 477
 DB 421 INIKGNMSGNRTANIKSLGSDIFCLSKEDLREVLSEYPAQITMEKKEIILLKMK 480
 QY 478 LDVNAEAEIALQAEATESRLRGDQDLDLOTKPARLAELESSALKIAYRIERLEMQR 537
 DB 481 LDVNAEAEIALQAEATESRLRGDQDLDLOTKPARLAELESSALKIAYRIERLEMQR 540
 QY 538 EWPMPEDLAEDDEGEPEEGTSKDEBGRASQEGPPE 575
 DB 541 EWPMPEDLAEDDEGEPEEGTSKDEBGRASQEGPPE 578

RESULT 13
 ADN38409
 ID ADN38409 standard; protein; 578 AA.
 XX
 AC ADN38409;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Novel human polynucleotide MO10a.
 XX
 KM anti-HIV; cytostatic; antiarteriosclerotic; antidiabetic; antiaesthetic;
 KM antiinflammatory; haemostatic; hypotensive; neuroprotective; anorectic;
 KM nootropic; antidepressant; immunosuppressive; antibacterial; vitruce;
 KM fungicide; protozoacide; tranquilizer; anticonvulsant; osteoprotic;
 KM analgesic; antiparkinsonian; dermatological; antifertility;
 KM cerebroprotective; antidiabetic; MOX-associated disorder;
 KM cardiomyopathy; atherosclerosis; diabetes; cell signal processing;
 KM metabolic pathway modulation; cancer; Von Hippel-Lindau syndrome;
 KM Alzheimer's disease; stroke; tuberos sclerosis; hypercalcaemia;
 KM Parkinson's disease; Huntington's disease; cerebral palsy; epilepsy;
 KM Leesh-Vyhan syndrome; multiple sclerosis; ataxia-telangiectasia;
 KM leukodystrophy; addiction; anxiety; depression; pain; obesity;
 KM Crohn's disease; osteoporosis; inflammatory bowel disease; infertility;
 KM hypertension; scleroderma; haemophilia; pancreatitis; autoimmune disease;
 KM asthma; arthritis; immunodeficiency; HIV; infection;
 KM graft-versus-host disease; gene therapy; vaccine; tissue typing;
 KM pharmacogenomic; human.

OS Homo sapiens.
 XX
 XX US2004029220-A1.
 XX
 PD 12-FEB-2004.
 XX
 PF 18-JUN-2002; 2002US-00174333.
 XX
 PR 26-APR-2000; 2000US-0200158P.
 PR 28-APR-2000; 2000US-0200613P.
 PR 28-APR-2000; 2000US-0200780P.
 PR 01-MAY-2000; 2000US-0201006P.
 PR 01-MAY-2000; 2000US-0201007P.
 PR 01-MAY-2000; 2000US-0201236P.
 PR 01-MAY-2000; 2000US-0201238P.
 PR 02-MAY-2000; 2000US-0201186P.
 PR 03-MAY-2000; 2000US-0201474P.
 PR 03-MAY-2000; 2000US-0201508P.
 PR 25-JUL-2000; 2000US-0220591P.
 PR 15-SEP-2000; 2000US-0232678P.
 PR 22-JAN-2001; 2001US-0263217P.
 PR 30-JAN-2001; 2001US-0265160P.
 PR 16-FEB-2001; 2001US-0265311P.
 PR 25-APR-2001; 2001US-00842758.
 PR 18-JUN-2001; 2001US-0298994P.
 PR 07-JUN-2002; 2002US-0366837P.
 XX
 PA (VERN/) VERNET C A M.
 PA (FERN/) FERNANDES E R.
 PA (GERL/) GERLACH V.
 PA (SHIM/) SHIMKETS R A.
 PA (MALY/) MALYANKAR U M.
 PA (BOLD/) BOLDOS F L.
 PA (ZERH/) ZERHUSEN B D.
 PA (SPYT/) SPYTEK K A.
 PA (MAJU/) MAJUMDER K.
 PA (TCHE/) TCHERNEV V T.
 PA (PADI/) PADIGARU M.
 PA (PAT/) PATIRAJAN M.
 PA (BURG/) BURGESS C E.
 PA (GANG/) GANGOLLI E A.
 PA (SMIT/) SMITHSON G.
 PA (RAST/) RASTELLI L.
 PA (MACD/) MACDOUGALL J R.
 PA (TAUP/) TAUPIER R J.
 PA (GROS/) GROSSE W M.
 PA (SZEK/) SZEKERES E S.
 PA (ALSO/) ALSOBROOK J P.
 PA (ANDE/) ANDERSON D W.
 PA (GUOX/) GUO X.
 PA (LILL/) LI L.
 PA (ZHON/) ZHONG M.
 PI Vernet CAM, Fernandes ER, Gerlach V, Shinkets RA, Malyankar UM;
 PI Boldos FL, Zehusen BD, Spytek KA, Majumder K, Tchernev VT;
 PI Padigan M, Patirajan M, Burgess CE, Gangolli EA, Smithson G;
 PI Rastelli L, MacDougall JR, Taupier RJ, Grose WM, Szekeres ES;
 PI Alsobrook JP, Anderson DW, Guo X, Li L, Zhong M;
 DR WPI; 2004-179668/17.
 DR N-PSDB; ADN38408.
 PT New isolated molecule (MOX) polypeptide, useful for diagnosing, treating
 PT or preventing MOX-associated diseases, such as infarction,
 PT atherosclerosis, diabetes, multiple sclerosis, Crohn's disease or cancer.
 XX
 XX Claim 1, SEQ ID NO 28; 212pp; English.
 CC The invention describes an isolated molecule (MOX) polypeptide. The MOX
 CC polypeptide, MOX nucleic acid and antibody are useful for treating,
 CC preventing or alleviating a MOX-associated disorder or a pathological
 CC state in a subject, particularly a human. In particular, the disorder is
 CC cardiomyopathy, atherosclerosis, diabetes, or a disorder related to cell

CC signal processing and metabolic pathway modulation. The MOIX polypeptide
CC and nucleic acid are also useful for diagnosing the presence of MOIX,
CC predisposition to a disease associated with altered levels of MOIX,
CC particularly cancer. The MOIX nucleic acid and polypeptide are especially
CC useful in the manufacture of a medicament for therapeutic or prophylactic
CC applications for disorders associated with aberrant MOIX expression or
CC activity, e.g. Von Hippel-Lindau syndrome, Alzheimer's disease, stroke,
CC tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's
CC disease, cerebral palsy, epilepsy, Lesch-Nyhan syndrome, multiple
CC sclerosis, ataxia-telangiectasia, leukodystrophies, addiction, anxiety,
CC depression, pain, obesity, Crohn's disease, osteoporosis, inflammation,
CC bowel disease, infertility, hypertension, scleroderma, hemophilia,
CC pancreaticitis, autoimmune disease, asthma, arthritis, immunodeficiencies,
CC HIV, viral, fungal, bacterial or protozoal infections, or graft-versus-
CC host disease. The DNA encoding the protein is useful in gene therapy for
CC treating the above conditions. This is the amino acid sequence of a novel
CC human MOIX polypeptide.

SQ Sequence 578 AA:

Query Match 98.9%; Score 2957.5; DB 8; Length 578;
Best Local Similarity 99.5%; Pred. No. 9.4e-275;

Matches 575; Conservative 0; Mismatches 0; Indels 3; Gaps 3;

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DB 1 MSODTKVKTTESSPPAPSKARRKLPLVLDPSGDYYWYNTNVPVWYNTLLVGRACP 60
QY 60 DLQHGVLAVMLVLDYTSDLLVLDWVVRPHT-GFLEOGILVVDKGRISRRYRTMSFLD 118
DB 61 DLQHGVLAVMLVLDYTSDLLVLDWVVRPHTGFGLEOGILVVDKGRISRRYRTMSFLD 120
QY 119 LASLPPTDVVYVRLGPHPTTLNLFRLAPRLFEAPDRTETRTAYPNARLAKMLYIFV 178
DB 121 LASLPPTDVVYVRLGPHPTTLNLFRLAPRLFEAPDRTETRTAYPNARLAKMLYIFV 180
QY 179 VHNMSCLYFALSRYLGFGRDAMVYPPDPAQGFEEFLRROYLSFEFSTLLITVGDTPPP 238
DB 181 VHNMSCLYFALSRYLGFGRDAMVYPPDPAQGFEEFLRROYLSFEFSTLLITVGDTPPP 240
QY 239 ARREBYLPMVGDFLIAVNGFATMGSSSVIYNNMTADAAFPDHALVKKYMKLQHVNRK 298
DB 241 ARREBYLPMVGDFLIAVNGFATMGSSSVIYNNMTADAAFPDHALVKKYMKLQHVNRK 300
QY 299 LERRVIDWYQHLQINKKMTNEVALIQLPERLRAEVANSVHLSTLSRVQIFQNCESATLE 358
DB 301 LERRVIDWYQHLQINKKMTNEVALIQLPERLRAEVANSVHLSTLSRVQIFQNCESATLE 360
QY 359 ELVLKLPQYTSPEGYVCRKGDIGQEMYIIRREGOLAVVADGITYAVLGAGLYFGEISI 418
DB 361 ELVLKLPQYTSPEGYVCRKGDIGQEMYIIRREGOLAVVADGITYAVLGAGLYFGEISI 420
QY 419 INIK-GNNSGNRRNTAKSLGSDLPCLSKEDLREVTSEYPOAQTIMEEKGREITLMMNK 477
DB 421 INIKGNNSGNRRNTAKSLGSDLPCLSKEDLREVTSEYPOAQTIMEEKGREITLMMNK 480
QY 478 LDVNAEAEIALQOATESRLGLDQDDLOTKPARLLAEBSALTIARIELENOTR 537
DB 481 LDVNAEAEIALQOATESRLGLDQDDLOTKPARLLAEBSALTIARIELENOTR 540
QY 538 EWPMPEDLAEDADGEPBEGETSKDEGRASQEGPGPE 575
DB 541 EWPMPEDLAEDADGEPBEGETSKDEGRASQEGPGPE 578
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RESULT 14

ID ADN38411 standard; protein; 575 AA.

AC ADN38411;

DT 17-JUN-2004 (first entry)

DE Novel human polynucleotide MO10b.

XX anti-HIV; cytostatic; antiarteriosclerotic; antidiabetic; antiasthmatic;
KW antiinflammatory; haemostatic; hypotensive; neuroprotective; anorectic;
KW nocotropic; antidepressant; immunosuppressive; antibacterial; virucide;
KW fungicide; protozoacide; tranquilizer; anticonvulsant; osteopathic;
KW analgesic; antiparkinsonian; dermatological; antinfertility;
KW cardiomyopathy; atherosclerosis; diabetes; cell signal processing;
KW cerebroprotective; antidiabetic; MOIX-associated disorder;
KW metabolic pathway modulation; cancer; Von Hippel-Lindau syndrome;
KW Alzheimer's disease; stroke; tuberous sclerosis; hypercalcaemia;
KW Parkinson's disease; Huntington's disease; cerebral palsy; epilepsy;
KW Lesch-Nyhan syndrome; multiple sclerosis; ataxia-telangiectasia;
KW leukodystrophy; addiction; anxiety; depression; pain; obesity;
KW Crohn's disease; osteoporosis; inflammatory bowel disease; infertility;
KW hypertension; scleroderma; haemophilia; pancreatitis; autoimmune disease;
KW asthma; arthritis; immunodeficiency; HIV; infection;
KW graft-versus-host disease; gene therapy; vaccine; tissue typing;
KW pharmacogenomic; human.

OS Homo sapiens.

PN US2004029220-A1.

PD 12-FEB-2004.

PE 18-JUN-2002; 2002US-00174333.

XX 26-APR-2000; 2000US-0200158P.
PR 28-APR-2000; 2000US-0200613P.
PR 28-APR-2000; 2000US-0200780P.
PR 01-MAY-2000; 2000US-0201006P.
PR 01-MAY-2000; 2000US-0201007P.
PR 01-MAY-2000; 2000US-0201236P.
PR 01-MAY-2000; 2000US-0201238P.
PR 02-MAY-2000; 2000US-0201186P.
PR 03-MAY-2000; 2000US-0201474P.
PR 03-MAY-2000; 2000US-0201508P.
PR 25-JUL-2000; 2000US-0220591P.
PR 15-SEP-2000; 2000US-0232678P.
PR 22-JAN-2001; 2001US-0263217P.
PR 30-JAN-2001; 2001US-0265160P.
PR 16-FEB-2001; 2001US-0269531P.
PR 25-APR-2001; 2001US-00842758.
PR 18-JUN-2001; 2001US-0298994P.
PR 07-JUN-2002; 2002US-0386837P.
XX

PA (VERN/) VERNET C A M.
PA (VERN/) FERNANDES E R.
PA (GERL/) GERLACH V.
PA (SHIM/) SHIMKETS R A.
PA (MALY/) MALYANKAR U M.
PA (BOLD/) BOLDOG F L.
PA (ZERR/) ZERRHUSEN B D.
PA (SPYT/) SPYTTER K A.
PA (MAUJ/) MAUDMER K.
PA (TCHER/) TCHERNIEV V T.
PA (PADJ/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (BURG/) BURGESS C E.
PA (GANG/) GANGOLLI E A.
PA (SMIT/) SMITHSON G.
PA (RAST/) RASTELLI L.
PA (MACD/) MACDOUGALL J R.
PA (TAUP/) TAUPIER R J.
PA (GROS/) GROSSE W M.
PA (SZER/) SZEKERES E S.
PA (ALSO/) ALSOEROOK J P.
PA (ANDE/) ANDERSON D W.
PA (GUOX/) GUO X.
PA (LITL/) LI L.
PA (ZHON/) ZHONG M.
XX

CC inhibitors. The polypeptides are also useful for identifying test
CC compounds which act as agonists or antagonists, for raising specific
CC antibodies, and as bait protein in a two-hybrid or three-hybrid assay
XX

Sequence 568 AA;

Query Match 96.7%; Score 2889; DB 6; Length 568;
Best Local Similarity 100.0%; Pred. No. 3.5e-268;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 14 RKLPLVLDPSGDYVYWMNTWTFPMVNLILIVCRACPPDLQHGIVAMLVLDYTSDLLX 73
QY 81 LLDVVRPHTGFLBEGILVVDKGRISRYVRTWSPFLDLASLMPDVVYVRLGPHPTTLR 140
Db 74 LLDVVRPHTGFLBEGILVVDKGRISRYVRTWSPFLDLASLMPDVVYVRLGPHPTTLR 133
QY 141 LNRFLRARPRLFEAFDRTETRTAYPNAFRIAKIMLYIFVVIHNSCLYFALSRYLGGRDA 200
Db 134 LNRFLRARPRLFEAFDRTETRTAYPNAFRIAKIMLYIFVVIHNSCLYFALSRYLGGRDA 193
QY 201 WVPDPAPQGPFRRLARQVLYSFYFSTLITTVGDTPPAREEYLPMVGDPLAVMGFAT 260
Db 194 WVPDPAPQGPFRRLARQVLYSFYFSTLITTVGDTPPAREEYLPMVGDPLAVMGFAT 253
QY 261 IMGSMSSVIYNNMTADAAFYPDHALVKKYMKLQHVNRKLERVIDMYOHLQINKKMTNEV 320
Db 254 IMGSMSSVIYNNMTADAAFYPDHALVKKYMKLQHVNRKLERVIDMYOHLQINKKMTNEV 313
QY 321 AILQHLPERLRAEVAVSVHLSTLSRVQIFQNCESLSELYKLQPTYSPEEYVCRKGD 380
Db 314 AILQHLPERLRAEVAVSVHLSTLSRVQIFQNCESLSELYKLQPTYSPEEYVCRKGD 373
QY 381 IGOEMYIIRBGLAVVADGGITQYAVLGAGLYFGEISIIINIKGNSGNRRTANIKSLGYS 440
Db 374 IGOEMYIIRBGLAVVADGGITQYAVLGAGLYFGEISIIINIKGNSGNRRTANIKSLGYS 433
QY 441 DLFCLSKEDLREVLSEYPOQTIMEKGREILLKNNKLDVNAEAAEIALQEATESRLRGL 500
Db 434 DLFCLSKEDLREVLSEYPOQTIMEKGREILLKNNKLDVNAEAAEIALQEATESRLRGL 493
QY 501 DQQLDDLQTKFARLLAELESSALKIAYRIERLEWOTREWPMPEDLAEDDGEPEEGTSK 560
Db 494 DQQLDDLQTKFARLLAELESSALKIAYRIERLEWOTREWPMPEDLAEDDGEPEEGTSK 553
QY 561 DEBGRASQGGPPGPE 575
Db 554 DEBGRASQGGPPGPE 568
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Search completed: February 10, 2005, 03:40:48
Job time : 95 secs

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OM protein - protein search, using sw model

Run on: February 10, 2005, 03:26:15 / Search time 27 Seconds
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Title: US-09-927-267-1
Perfect score: 2989
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Scoring table: BLOSUM62
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Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
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6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1549.5	51.8	694	US-09-538-092-1351	Sequence 1351, Ap
2	1538.5	51.5	686	US-09-538-092-1037	Sequence 1037, Ap
3	1526.5	51.1	690	US-09-275-252A-19	Sequence 19, Appl
4	847	28.3	261	US-09-275-252A-18	Sequence 18, Appl
5	719	24.1	909	US-09-538-092-1315	Sequence 1315, Ap
6	488	16.3	129	US-08-997-685A-46	Sequence 46, Appl
7	475.5	15.9	126	US-08-997-685A-57	Sequence 57, Appl
8	468.5	15.7	126	US-08-997-685A-58	Sequence 58, Appl
9	466.5	15.6	528	US-08-997-685A-4	Sequence 4, Appl
10	457.5	15.3	504	US-09-086-436-33	Sequence 33, Appl
11	454.5	15.2	597	US-09-086-436-41	Sequence 41, Appl
12	450.5	15.1	597	US-08-997-685A-12	Sequence 12, Appl
13	441.5	14.8	749	US-08-997-685A-10	Sequence 10, Appl
14	441.5	14.8	710	US-09-086-436-39	Sequence 39, Appl
15	441.5	14.8	949	US-08-997-685A-2	Sequence 2, Appl
16	441.5	14.8	910	US-09-086-436-31	Sequence 31, Appl
17	421.5	14.1	506	US-09-086-436-35	Sequence 35, Appl
18	420.5	14.1	506	US-08-997-685A-6	Sequence 6, Appl
19	406	13.6	170	US-09-358-383C-27	Sequence 27, Appl
20	402	13.4	319	US-09-358-383C-22	Sequence 22, Appl
21	391	13.1	962	US-09-614-480-9	Sequence 9, Appl
22	391	13.1	962	US-09-694-777A-3	Sequence 3, Appl
23	391	13.1	962	US-10-422-075-9	Sequence 9, Appl
24	387.5	13.0	960	US-09-694-777A-21	Sequence 21, Appl
25	387.5	13.0	962	US-09-694-777A-24	Sequence 24, Appl
26	382.5	12.8	1284	US-09-343-494-9	Sequence 9, Appl
27	382.5	12.8	1284	US-09-358-383C-11	Sequence 11, Appl

28	380.5	12.7	989	US-09-694-777A-4	Sequence 4, Appl
29	380	12.7	1083	US-09-600-776-2	Sequence 2, Appl
30	380	12.7	1083	US-09-343-494-1	Sequence 1, Appl
31	379	12.7	1083	US-09-358-383C-2	Sequence 2, Appl
32	377	12.6	987	US-09-694-777A-22	Sequence 22, Appl
33	377	12.6	989	US-09-694-777A-23	Sequence 23, Appl
34	377	12.6	1082	US-09-336-643A-20	Sequence 20, Appl
35	376.5	12.6	988	US-09-614-480-2	Sequence 2, Appl
36	376.5	12.6	988	US-10-162-012-5	Sequence 5, Appl
37	376.5	12.6	988	US-10-422-075-2	Sequence 2, Appl
38	376.5	12.6	1107	US-09-358-383C-16	Sequence 16, Appl
39	375	12.5	1159	US-08-956-242-13	Sequence 13, Appl
40	375	12.5	1159	US-09-351-215-13	Sequence 13, Appl
41	375	12.5	1159	US-09-226-012-2	Sequence 2, Appl
42	375	12.5	1159	US-09-226-012-4	Sequence 4, Appl
43	375	12.5	1159	US-09-358-383C-10	Sequence 10, Appl
44	375	12.5	1159	US-09-275-252A-12	Sequence 12, Appl
45	370.5	12.4	888	US-08-956-242-4	Sequence 4, Appl

ALIGNMENTS

```
RESULT 1
US-09-538-092-1351
; Sequence 1351, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Glot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuratSeqFormatter Version 0.9
; SEQ ID NO 1351
; LENGTH: 694
; TYPE: prt
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number Q16281
US-09-538-092-1351
Query Match          51.8%; Score 1549.5; DB 4; Length 694;
Best Local Similarity 52.6%; Pred. No. 11e-147;
Matches 290; Conservative 112; Mismatches 140; Indels 9; Gaps 2;
9 TSSPPAPSKARKLPLVLDPSGDYYWMLNMPVWNLIIIVCRACFPDLOHGYVA 68
Db 143 TSNMTEERKTKKQDAIVDPSSNLYRMNLTAIPVYNNWLLCRACFDLOSEYIML 202
Qy WIVLDYTDLLYLDMVVRFHGTGLEGLIVVDKRISSRYRTWSFFLDLASLMDPTDV 128
203 WIVLDYSADVLVVLVLRARFGFLEOGLMWSDTNRLQHYKTTQFQKLDVLSLPTDIA 262
Qy VYRLGPHPTPLRLNFLAPRLFEAPDTERRTAPNAPRLAKMLYIFVVIHMSCLYF 188
263 YLKVTNPEVVENFLKFSRLFEFDTRTKTNPNMFRIGNLVLIILHMACTYF 322
Qy 189 ALSRLGFGRDAMVVPDPAQGFERLIRQYLYSFSTLIITTVGDTPPPAEEBYLFMV 248
323 AISKRTIGCTDSWVYVNPISIPHGRLSKRTIYSLWSTLTITLTIGETPPVDEBYLFV 382
Qy 249 GDFLLAVNGFATIKWSMGSVYNNMTADAPYPDHALYKRYKMLQHNKLERRYITDYO 308
383 VDFLLGVILFATIVNGVSMISNMNASRAEFQAKIDSIKQYQFRKVKTDLETRVIRWFD 442
Db
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      443  YLMANKTVDKEVLEKSLPKLKEKELAINVHDLTKKVRIFODEAGLVELVLTQKRPV 502
QY      369  YSPREYCRKGDIGQEMYYIIRREGQAVAVDDGITQYAVLAGLYFGESIIINIKGNMGN 428
      503  FSPEDYICRKGDIQKEMYYIINEGKLAVADDGVITQFVVLSDGSYFGEISILINIKGSKN 562
QY      429  RRTANIKSLGYSDLPCLSKEDLEEVLYSEYPOAQTIEMERKEIILKNKRLDVNAEAEIA 488
      563  RRTANIKSIGSDLPCLSKEDLMEALTEPEAKKALBEKGRQILMKDNLIDEELARAG-A 621
QY      489  LQEALESRLRGDQDQDLDTQTKPARLLAELESSALKIAYRIERLEWOTR-----EWP 540
      622  DPEDEKRYQQLSSSLDITLQTRFARLLAEYNATQMKQKRLQLESQVKGGDKPLADGE 681
QY      541  MPEDLAEDDE 551
      682  VPGDATKTEBK 692

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RESULT 2
US-09-538-092-1037
; Sequence 1037, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Glot, Loic
; APPLICANT: Manfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 1037
; LENGTH: 686
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number P23973
US-09-538-092-1037

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Query Match      51.5%; Score 1538.5; DB 4; Length 686;
Best Local Similarity 54.0%; Pred. No. 1.4e-146;
Matches 285; Conservative 113; Mismatches 129; Indels 1; Gaps 1;

QY      6  KVTTESSPPAPSKARKLLPVLDPGSDYYWMLNTWVPVWYNIILIVCRACFPDLOHGY 65
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QY      66  LVAMLVLDYTSDDLVLIDMVVRFHTGFLGEGILVVDKGRISRRYRTMSFFDLASLMP 125
      193  LEYWLILDYSDIYLLIDMFVTRTGYLGEGLVKEELKINKKSNLQFGLDVLSLPT 252
QY      126  DVVYVRLGPHPTPLRLNRLFLAPRLFEAFDRTETRTAYPNAFRIAKMLYIFVVIHNSC 185
      253  DLYFLKGMWYPEIRLNLRLFRSMFEFFQRTERTYNNIFRISNLVMTIIVIIHNNAC 312
QY      186  LVFALSRYLGFGRDAMVYPPDPAQGFERLROLYISFYFSTLILTTVGDTPPAREEYL 245
      313  VFYSISALIGFNDTWYPPDINDPEFGLARKVYSLYWSLTLTLTTIGETPPVRDSEYV 372
QY      246  FVWGDFLLAVMGFATIGMSMSVLYNNMTADAAPYDPHALVKKYMKLOHNRKLEERYID 305
      373  FVVVDFLIGVLIFFATIVGNISMSINNNARAEFORAIDAIKOYMFRRNSKOMERKVIK 432

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QY      306  WYOHQINKMTNEVAIIQHLPERLRAEVAVSVHLSTLSRVQIFONCEASLLEELVLTQ 365
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QY      366  POTSPGEYVCRKGDIGQEMYYIIRREGQAVAVDDGITQYAVLAGLYFGESIIINIKGNM 425
      493  POTSYPGDYICRKGDIQKEMYYIIRREGKLAVADDGVITQFVVLSDGSYFGEISILINIKSK 552
QY      426  SGNRTANIKSLGYSDLPCLSKEDLEEVLYSEYPOAQTIEMERKEIILKNKRLDVNAEAA 485
      553  AGNRTANIKSIGSDLPCLSKEDLMEALTEPEAKKALBEKGRQILMKDNLIDEELARAG-A 612
QY      486  EIALQEALESRLRGDQDQDLDTQTKPARLLAELESSALKIAYRIERLE 533
      613  GSDPD-LBEKVTREKSGVDLQTRFARLLAEYSEMOQKRLQRLTYE 659

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RESULT 3
US-09-275-252A-19
; Sequence 19, Application US/09275252A
; Patent No. 6641997
; GENERAL INFORMATION:
; APPLICANT: MacKinnon, Roderick
; APPLICANT: The Rockefeller University
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
; TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
; FILE REFERENCE: 018512-00290105
; CURRENT APPLICATION NUMBER: US/09/275,252A
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: US 09/045,529
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/054,347
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: WO PCT/US99/06307
; PRIOR FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-275-252A-19

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Query Match      51.1%; Score 1526.5; DB 4; Length 690;
Best Local Similarity 53.8%; Pred. No. 2.3e-145;
Matches 284; Conservative 112; Mismatches 131; Indels 1; Gaps 1;

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      137  KKKKEKSKDKKEHKKKEVVVIDPSGNTYNNLFCITLPVWYNTWYIARACFDELQSDY 196
QY      66  LVAMLVLDYTSDDLVLIDMVVRFHTGFLGEGILVVDKGRISRRYRTMSFFDLASLMP 125
      197  LEYWLILDYSDIYLLIDMFVTRTGYLGEGLVKEELKINKKSNLQFGLDVLSLPT 256
QY      126  DVVYVRLGPHPTPLRLNRLFLAPRLFEAFDRTETRTAYPNAFRIAKMLYIFVVIHNSC 185
      257  DLYFLKGMWYPEIRLNLRLFRSMFEFFQRTERTYNNIFRISNLVMTIIVIIHNNAC 316
QY      186  LVFALSRYLGFGRDAMVYPPDPAQGFERLROLYISFYFSTLILTTVGDTPPAREEYL 245
      317  VFYSISKALIGFNDTWYPPDINDPEFGLARKVYSLYWSLTLTLTTIGETPPVRDSEYV 376
QY      246  FVWGDFLLAVMGFATIGMSMSVLYNNMTADAAPYDPHALVKKYMKLOHNRKLEERYID 305
      377  FVVVDFLIGVLIFFATIVGNISMSINNNARAEFORAIDAIKOYMFRRNSKOMERKVIK 436
QY      306  WYOHQINKMTNEVAIIQHLPERLRAEVAVSVHLSTLSRVQIFONCEASLLEELVLTQ 365
      437  WEDYLMTKKYVDEKVKLYLPDKLRARIAINVHDLTKKVRIFADCGAGLVELVLTQ 496
QY      366  POTSPGEYVCRKGDIGQEMYYIIRREGQAVAVDDGITQYAVLAGLYFGESIIINIKGNM 425

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Db 497 PQVSPGGYICKGKGGIGEMWITIKGKGLAVADDEVTOFVVLSDSTGEISILNIKSK 556
Qy 426 SGNRTANIKSLGSDFLCLESKEDREVLSYPOAQOTMEKGRILLKANKLDVNAEA 485
Db 557 AGNRTANIKSIGSDFLCLESKEDREVLSYPOAQOTMEKGRILLKANKLDVNAEA 616
Qy 486 EIALQATERSRLRGDQDLQOTKFAFLAELESSALKINRIERLE 533
Db 617 GSDPKD-LEEVTRMEGSDVLQTRFARILAEESMOQLKORLTKE 663

RESULT 4

US-09-275-252A-18
; Sequence 18, Application US/09275252A
; Patent No. 664197
; GENERAL INFORMATION:
; APPLICANT: MacKinnon, Roderick
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
; TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
; TITLE OF INVENTION: Channel Proteins, and Uses Thereof
; FILE REFERENCE: 018512-002901US
; CURRENT FILING DATE: 1999-03-24
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: US 09/045,529
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/054,347
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: WO PCT/US99/06307
; PRIOR FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 18
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-275-252A-18

Query Match 28.3%; Score 847; DB 4; Length 261;

Best Local Similarity 59.8%; Pred. No. 3.5e-77;

Matches 156; Conservative 52; Mismatches 53; Indels 0; Gaps 0;

Qy 186 LYLALSRLLGRGRDMMVYDPAQPGFERLRQYLSFYFSTLLITTVGDPPEAREEYL 245
Db 1 LYLALSRLLGRGRDMMVYDPAQPGFERLRQYLSFYFSTLLITTVGDPPEAREEYL 60
Qy 246 FMVGDFLAVMGFATINGSMSVIVNNTADAFYPDHALVKKYMKLQHVNKLEBRVID 305
Db 61 FVIFPFLIGVILFATIVGVSMISMANTRAPEFOAKIDAVGHVQFRVSKGMEAKYIR 120
Qy 306 WYQHLQINKKMTNEVAIIQHLPERLRAEYAVSVHLSTSRVOIFONCEASLLEELVCLKQ 365
Db 121 WEDVMTWKKTVDEREILLKNIPLAKRAEIAIVNHLSTLKVRIIFHDCEAGLLVELVKLR 180
Qy 366 POTVSPGVYVCKGKIGQEMYIRREGQLAVVADDTQYAVGAGIXPEISIIINIKGM 425
Db 181 POFVSPGVYVCKGKIGQEMYIRREGQLAVVADDTQYAVGAGIXPEISIIINIKGSK 240
Qy 426 SGNRTANIKSLGSDFLCLES 446
Db 241 MGNRTANIRSLGSDFLCLES 261

RESULT 5

US-09-538-092-1315
; Sequence 1315, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Glot, Loic
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542

; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuratSeqFormatter Version 0.9
; SEQ ID NO 1315
; LENGTH: 909
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)-(0)
; OTHER INFORMATION: Polypeptide Accession Number Q14028
US-09-538-092-1315

Query Match 24.1%; Score 719; DB 4; Length 909;

Best Local Similarity 29.6%; Pred. No. 2.7e-63;

Matches 187; Conservative 125; Mismatches 227; Indels 92; Gaps 19;

Qy 4 DTKYTTSSP-----PAP-SKARKLPLV----- 26
Db 246 DEDVTSDESPSPSPAKKAPAPDPPTKPAEAPVEEHHYCDMLCKFKRHPWKYQFPQS 305
Qy 27 LDP-SGDYVWMLNMFPPVWYLLIYCRACFPDLQGVIVAMVILDTSDLYLDMV 85
Db 306 IDPLNLMVLMVLFVVAAMNMCWILVRAVFPQTPDNTHHMLMDLYLCLDLYFLDT 365
Qy 86 VRFHT--GFLQGLIVDKRISRYVTFWFFLDIASLPTDVVYVRLGPTPTLRNR 143
Db 366 V-FQTRLOPVAGGDIITTKOMRNNYLSKRFKMDLSLLPLDPLYLKGVN-PLRLRPR 423
Qy 144 FLRPLRLEADRTETRTAVPNAFRIAKMLYEVVHNSCLYFALSRYLFGSDAVY 203
Db 424 CLKVAFPEFNSRLSISLKAIVYVIRTVLTLNSCLYVWASAGYGLSGSTHWY 483
Qy 204 PDPAPGFERLRQYLSFYFSTLLITTVGDPPEAREEYLFMVGDFLAVMGFATIMG 263
Db 484 -----DGVGNSIRCYFAVKTLLITIGLPDKTLPELVFQLNFTGVFAFSVMIG 535
Qy 264 SMSVIVNNTADAFY---PDHALVKKYMKLQHVNKLEBRVIDMYOHLQINKKMTNEV 320
Db 536 QMRDVP--GAATRGQYTVSCHKDSTY--KYNMFYKPKVQVQKRYVETWHSQGLDES 592
Qy 321 ALOHLPERLRAEYAVSVHLSTSRVOIFONCEASLLEELVCLKQPOYSPGVYCKKD 380
Db 593 ELMVQLPDKMRDLDAIDVNVIVSKVALFQCGCDROMIFDMLKRLSVVYLPMDYVCKKGE 652
Qy 381 IGOEMYITREGQLAVV-ADDTQYAVGAGIXPEISIIINIKGMNGNRTANIKSLGY 439
Db 653 IGRVYIIOAQGVQVLAGSDGKSVLVTLKAGSVFSEISLLAVGG--GNRTANVAVAGF 709
Qy 440 SDLFCLSKEDREVLSYPOAQOTMEKGRILLKANKLDVNAEAELALOE----- 491
Db 710 TNLFLIDKDLNELLVHNPESQKLRKARLBRNNK--PREESVILIPPRAGTPKLF 767
Qy 492 ----ATESRLRGDQDLQOTKFAFLAE-ESSALKIAYRIERLEQTRMPEBIDA 546
Db 768 NAALMTGKMGKAK-----GKLAHLRALRLELAALBAAGHEBELVQ-----A 813
Qy 547 EADDEGEPEEGSKDEBGRASOEG---PPGP 574
Db 814 KSSODVKGEGSAAPDQHTHPKEAATDPAP 844

RESULT 6

US-08-997-685A-46
; Sequence 46, Application US/08997685A
; Patent No. 6551821
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University

Query Match	15.9%;	Score 475.5;	DB 4;	Length 126;
Best Local Similarity	71.7%;	Pred. No. 4.7e-40;		
Matches 91; Conservative	20;	Mismatches 15;	Indels 1;	Gaps 1.

RESULT 9
 US-08-997-685A-4
 ; Sequence 4, Application US/08997685A
 ; Patent No. 6551821
 ; GENERAL INFORMATION:
 ; APPLICANT: The Trustees of Columbia University
 ; APPLICANT: Kandell, Eric
 ; TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof

FILE REFERENCE: 0575/54806
 CURRENT APPLICATION NUMBER: US/08/997,685A
 CURRENT FILING DATE: 1997-12-12
 NUMBER OF SEQ ID NOS: 60
 SOFTWARE: Patentin version 3.1
 SEQ ID NO 4
 LENGTH: 528
 TYPE: PRT
 ORGANISM: mouse;
 PUBLICATION INFORMATION:
 DATABASE ACCESSION NUMBER: AAC40125
 DATABASE ENTRY DATE: 1998-05-29
 RELEVANT RESIDUES: (1)..(504)
 US-08-997-685A-4

Query Match 15.6%; Score 466.5; DB 4; Length 528;
 Best Local Similarity 25.3%; Pred. No. 4,3e-38;
 Matches 122; Conservative 109; Mismatches 202; Indels 49; Gaps 12;

QY 26 VLDPSGDYVWMNTMVPVWYNIILVCRACFPDLQHGVLVAMLVLDYSDLYLDMV 85
 DB 27 IHPYSDRFRFYWDFMLFMVGNLIIVGITE--FKDETTAPWIVFVNSDTEFLMDLV 84
 QY 86 VRFHTGFL--EGGILVVDKGRISRYVWTWSEFLDLASIMPTDYYV-----129
 DB 85 INFRTGIVIEDTEIILDEPKIKKKYKRTW-FVDFVSSIPVDYIFLVEKGIDSEVYKT 143
 QY 130 ---VRLGHTPTLRLNRLRFLRPLRPEAFDRT-----TRTAVPNAFRIAKMLYIFVVIH 181
 DB 144 ARAIRIVFTKILSLRLRLRLRLRYIHQWEIEFHTYDLASAVMRICNLISMMLLCH 203
 QY 182 WNSCLYFALSRYLGFGRDAWVYPPDAQPGFERLRQY--LYSF---YFSTLILTTVGD 235
 DB 204 WDGCLOFLVPMLODPSPDCWVSIN-----NMVNSWSELYSFALFKAMSHMLCIGYGRQ 257
 QY 236 PPPAREEYLFMVNGDFLLAVMGFATMGSMSSVYINMTADAIFYPDHALVKKYKLOHV 295
 DB 258 APESMTDITLMTL-SMIVGATCYAMFIGHATLQSLDSRRQYQYQYQVQMSFHL 316
 QY 236 NRKLRVYIDWYQHLQINKKMTNEVAIIQHLPERLRAEVAVSHLSTSRVOIFONCEAS 355
 DB 317 PADFRQKIHDIYEH-RYQGRKMSDEDSILGELNGPLREBEIVNFCRKLVSMPLEFANADPN 375
 QY 356 LLEBLVLYLQPTYSRGEYVCKDIOGEMYIIRBQGLAVVADGITQYAVLGAAGLYFGE 415
 DB 376 FYTAMLTLYLKFEVFPQGDYIIRBGTIGKMYFIQGVVSVLYKG--NKEMKLSDSGYFGE 433
 QY 416 ISIIINIKMGMSGNRRITANKISLGYSDLPCLSKEDLREVLSEYPOAQTMEEGREIILKM 475
 DB 434 ICL-----LTRGRITASVRADTYCRLYSLVDNFEVLEETPMRRARETVVAIDRLRI 487
 QY 476 NK 477
 DB 488 GK 489

RESULT 10
 US-09-086-436-33
 Sequence 33, Application US/09086436
 Patent No. 6703485
 GENERAL INFORMATION:
 APPLICANT: Kandel, Eric R.
 APPLICANT: Santoro, Bina
 APPLICANT: Bartsch, Dusan
 APPLICANT: Siegelbaum, Steven
 APPLICANT: Tibbs, Garech
 APPLICANT: Grant, Seth
 TITLE OF INVENTION: Brain or Heart Cyclic Nucleotide Gated Ion Channel and
 TITLE OF INVENTION: Uses Thereof
 FILE REFERENCE: 0575/54806-A
 CURRENT APPLICATION NUMBER: US/09/086,436
 CURRENT FILING DATE: 1998-05-28
 NUMBER OF SEQ ID NOS: 67

SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO 33
 LENGTH: 504
 TYPE: PRT
 ORGANISM: Murine
 US-09-086-436-33

Query Match 15.3%; Score 457.5; DB 4; Length 504;
 Best Local Similarity 25.1%; Pred. No. 3,3e-37;
 Matches 121; Conservative 109; Mismatches 203; Indels 49; Gaps 12;

QY 26 VLDPSGDYVWMNTMVPVWYNIILVCRACFPDLQHGVLVAMLVLDYSDLYLDMV 85
 DB 27 IHPYSDRFRFYWDFMLFMVGNLIIVGITE--FKDETTAPWIVFVNSDTEFLMDLV 84
 QY 86 VRFHTGFL--EGGILVVDKGRISRYVWTWSEFLDLASIMPTDYYV-----129
 DB 85 INFRTGIVIEDTEIILDEPKIKKKYKRTW-FVDFVSSIPVDYIFLVEKGIDSEVYKT 143
 QY 130 ---VRLGHTPTLRLNRLRFLRPLRPEAFDRT-----TRTAVPNAFRIAKMLYIFVVIH 181
 DB 144 ARAIRIVFTKILSLRLRLRLRLRYIHQWEIEFHTYDLASAVMRICNLISMMLLCH 203
 QY 182 WNSCLYFALSRYLGFGRDAWVYPPDAQPGFERLRQY--LYSF---YFSTLILTTVGD 235
 DB 204 WDGCLOFLVPMLODPSPDCWVSIN-----NMVNSWSELYSFALFKAMSHMLCIGYGRQ 257
 QY 236 PPPAREEYLFMVNGDFLLAVMGFATMGSMSSVYINMTADAIFYPDHALVKKYKLOHV 295
 DB 258 APESMTDITLMTL-SMIVGATCYAMFIGHATLQSLDSRRQYQYQYQVQMSFHL 316
 QY 236 NRKLRVYIDWYQHLQINKKMTNEVAIIQHLPERLRAEVAVSHLSTSRVOIFONCEAS 355
 DB 317 PADFRQKIHDIYEH-RYQGRKMSDEDSILGELNGPLREBEIVNFCRKLVSMPLEFANADPN 375
 QY 356 LLEBLVLYLQPTYSRGEYVCKDIOGEMYIIRBQGLAVVADGITQYAVLGAAGLYFGE 415
 DB 376 FYTAMLTLYLKFEVFPQGDYIIRBGTIGKMYFIQGVVSVLYKG--NKEMKLSDSGYFGE 433
 QY 416 ISIIINIKMGMSGNRRITANKISLGYSDLPCLSKEDLREVLSEYPOAQTMEEGREIILKM 475
 DB 434 ICL-----LTRGRITASVRADTYCRLYSLVDNFEVLEETPMRRARETVVAIDRLRI 487
 QY 476 NK 477
 DB 488 GK 489

RESULT 11
 US-09-086-436-41
 Sequence 41, Application US/09086436
 Patent No. 6703485
 GENERAL INFORMATION:
 APPLICANT: Kandel, Eric R.
 APPLICANT: Santoro, Bina
 APPLICANT: Bartsch, Dusan
 APPLICANT: Siegelbaum, Steven
 APPLICANT: Tibbs, Garech
 APPLICANT: Grant, Seth
 TITLE OF INVENTION: Brain or Heart Cyclic Nucleotide Gated Ion Channel and
 TITLE OF INVENTION: Uses Thereof
 FILE REFERENCE: 0575/54806-A
 CURRENT APPLICATION NUMBER: US/09/086,436
 CURRENT FILING DATE: 1998-05-28
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO 41
 LENGTH: 597
 TYPE: PRT
 ORGANISM: Human
 US-09-086-436-41

Query Match 15.2%; Score 454.5; DB 4; Length 597;


```
QY 237 PPARBEEYLFWVGDFLAVMGFATIMGSSSVIYMMNTADAAFYDPHALVKKMKLQHYN 296
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 245 PVSMDLMTIML-SMIVGATCYAMFVGHAITALIQSLDSRRQYQEKYQVEGYMSPFKLP 303
QY 297 RULERVVDIMYQHLQINKMKNTEVAILOHLPERLBAEVAVSHLSVQIFQNCASL 356
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 304 ADMRKIDHYEH-RYQGIPEENILNELNDPLREELVNFNCRKLVATMPLFANADPWF 362
QY 357 LEEVLKLOPQYSPGEYVCRKDIGOEYIIREGOLAVVADGITQYAVLAGLYPEEI 416
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 363 VTAMLSKLRFEVFOGDIYIREGAVGKKMYFIQHGAVGYTS--SKEMKLTDSYFGEI 420
QY 417 SIINKMGSGNRRTANKISLGSDLFCLSKEDLREVISEYFOAQTIME----- 466
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 421 CLLT-KG-----RTASVRADYTCRLYSLSVDNFEVLEEYPMRRAPETVAIDRLRIG 474
QY 467 KGREILLKMKLQDVN 481
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 475 KKNSTILQKFOKDLN 489
```

RESULT 14

```
US-09-086-436-39
; Sequence 39, Application US/09086436
; Patent No. 6703485
; GENERAL INFORMATION:
; APPLICANT: Kandel, Eric R.
; APPLICANT: Santoro, Bina
; APPLICANT: Bartsch, Dusan
; APPLICANT: Siegelbaum, Steven
; APPLICANT: Tibbs, Garech
; APPLICANT: Grant, Seth
; TITLE OF INVENTION: Brain or Heart Cyclic Nucleotide Gated Ion Channel and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 05/5/54806-A
; CURRENT APPLICATION NUMBER: US/09/086,436
; CURRENT FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 39
; LENGTH: 749
; TYPE: PRT
; ORGANISM: Human
US-09-086-436-39
```

Query Match 14.8%; Score 441.5; DB 4; Length 749;

Best Local Similarity 24.2%; Pred. No. 2.7e-35;

Matches 120; Conservative 116; Mismatches 202; Indels 57; Gaps 15;

```
QY 26 VLDPESGDYYMMMLNMFVPMVYNIILIVGRACFPDLQHGIVLAVMLVDYTSPLLYLLMV 85
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 13 IIPYSDFRFYVDLIMLMVGNLVIIPVGTFF--FTEGTTTPMIIFNVASDVFLLDLIT 70
QY 86 VAFHTGFL--EKGILVNDKGRISRYVWTSPFLDASIMPTDVY----- 129
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 71 MNFRGTGTVNDESEIILPKVIXKMYIKSW-FVDFISSIPDYIFLIVEKGMDESEYKT 129
QY 130 ---VFLGPHPTPLRLNRLRPLF-----EAFDRT-ETRTAVPNAFRAKMLYIFV 178
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 130 ARAARIVFTFKLISLRILRLRLRYIHQWEIIFHMYIDLASAVVRIENLIGMML---L 186
QY 179 VTHMNSCLYFALSRILGFGDAMVYDPDAPQGFEBRLRQYLSFY--FSTLLTLTVGDT 236
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 187 LCHMGCLQFLVPLIADFPDPCWVSLN--EMVNDKSGKYSTALFRAMSHMLCIGYQAO 244
QY 237 PPARBEEYLFWVGDFLAVMGFATIMGSSSVIYMMNTADAAFYDPHALVKKMKLQHYN 296
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 245 PVSMDLMTIML-SMIVGATCYAMFVGHAITALIQSLDSRRQYQEKYQVEGYMSPFKLP 303
QY 297 RULERVVDIMYQHLQINKMKNTEVAILOHLPERLBAEVAVSHLSVQIFQNCASL 356
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 304 ADMRKIDHYEH-RYQGIPEENILNELNDPLREELVNFNCRKLVATMPLFANADPWF 362
```

```
QY 357 LEEVLKLOPQYSPGEYVCRKDIGOEYIIREGOLAVVADGITQYAVLAGLYPEEI 416
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 363 VTAMLSKLRFEVFOGDIYIREGAVGKKMYFIQHGAVGYTS--SKEMKLTDSYFGEI 420
QY 417 SIINKMGSGNRRTANKISLGSDLFCLSKEDLREVISEYFOAQTIME----- 466
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 421 CLLT-KG-----RTASVRADYTCRLYSLSVDNFEVLEEYPMRRAPETVAIDRLRIG 474
QY 467 KGREILLKMKLQDVN 481
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 475 KKNSTILQKFOKDLN 489
```

RESULT 15

```
US-08-997-685A-2
; Sequence 2, Application US/08997685A
; Patent No. 6551821
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University
; APPLICANT: Kandel, Eric
; TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof
; FILE REFERENCE: 05/5/54806
; CURRENT APPLICATION NUMBER: US/08/997,685A
; CURRENT FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 2
; LENGTH: 910
; TYPE: PRT
; ORGANISM: mouse
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (130)..(148)
; OTHER INFORMATION: S1
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (164)..(185)
; OTHER INFORMATION: S2
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (208)..(229)
; OTHER INFORMATION: S3
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (243)..(271)
; OTHER INFORMATION: S4
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (291)..(313)
; OTHER INFORMATION: S5
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (332)..(358)
; OTHER INFORMATION: P
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (367)..(387)
; OTHER INFORMATION: S6
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (472)..(602)
; OTHER INFORMATION: CNB
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AAC53518
; DATABASE ENTRY DATE: 1997-12-27
; RELEVANT RESIDUES: (1)..(910)
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US-08-997-685A-2

Query Match 14.8%; Score 441.5; DB 4; Length 910;

Best Local Similarity 24.2%; Pred. No. 3.7e-35;

Matches 120; Conservative 116; Mismatches 202; Indels 57; Gaps 15;

QY 26 VLDPGSDYYWMLNTMFPVWMLIIIVCRACFPDLQHGVLVAMLVLDYSDLYLDMV 85
 Db 123 IIHPSDFRFPYDMLIMIMWGNLVIIPVGITF--FTEQTTPIIFNVASDTVFLDLII 180
 QY 86 VRFHTGFL--EGLIIVDKRISRRYRTWSPFLDLASIMPTVVY----- 129
 Db 181 MNFRGTVNEDSEIILDPKVIKKNYLSKW-FVVDFISSIPVDYIFLIVEKGMDEVYKT 239
 QY 130 ---VPLGPHTPILNRFLRRLF-----EAFDRF-EFRTAEPNAPRIAKMLYIFV 178
 Db 240 ARALEIVRFTKLISLRILRLIRYIHQWBEIFHMTYDLASAVRIIFNLIGMML--L 296
 QY 179 VIHMNSCLYFALSRYLGFGRDAMVYPDPAPGFERLRROYLSFY--FSTLILTTVGDP 236
 Db 297 LCHWDGCIQFLVPLIQLDFPPDCWGLN--EMVNDSWGQYSYALFKASHMLCIGYGAQ 354
 QY 237 PPAREEYLFVVGDFLLAVMGFATIMGSMSVYINMNTADAAFYPDHALVKKYMKLQHVN 296
 Db 355 FVMSMDLWITML-SMIVGATCYAMFVGHATALIQSLDSSRRQYQEKYQVEQYMSFHKLP 413
 QY 297 RKLERRVIDWYOHLOINKMTNEVALLOHLPERLRBAVAVSVHLSTLSRVQIFQNCESL 356
 Db 414 ADMROKIHDIYEH-RYQGIPEENILSELNDPLREBITVENCRLVAMPLFANADPNF 472
 QY 357 LBEIVLKLQPTVSPGEYVCRKDIQOENYIIRBQLAVVADGITOYAVLGAGLYFGEI 416
 Db 473 VTAMLSKLRFEVFGQGDYIIRGAVGKMYFIQHGVAGVITKS--SKEMKLDGSPGEI 530
 QY 417 SIINKMNSGNRRPANIKSIGYDLPCLSKEDLREVLSEYPOAQTIME----- 466
 Db 531 CLLT-KG-----RRTASVADTYCRLYSISVDNFNEVLSEYPMRRARAFETVAIDRLDRIG 584
 QY 467 KGREILLKMKLDPVN 481
 Db 585 KKNSTILQKQKDLN 599

Search completed: February 10, 2005, 03:45:00
 Job time : 28 secs

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OM protein - protein search, using sw model

Run on: February 9, 2005, 20:51:50 ; Search time 111 Seconds

(without alignments)
2980.544 Million cell updates/sec

Title: US-09-927-267-1

Sequence: 1 MSQDKVKTSTSSPPAPSKA.....EGTSKDEGRASQEGPPGPE 575

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_prot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2811	94.0	575	1 CNGX_RAT	Q64359 ratu...
2	2118	70.9	474	2 O81V77	Q81V77 homo sapien
3	1638.5	54.8	609	2 O8JFPO	O8JFPO ictalunus p
4	1585.5	53.0	551	2 O8JFPO	O8JFPO ictalunus p
5	1582.5	52.9	631	2 O8CFV6	O8CFV6 mus musculu
6	1579	52.8	706	1 CNG3_BOVIN	Q29441 bos taurus
7	1578	52.8	611	2 O9QW7	O9QW7 ratu...
8	1578	52.8	632	2 O9ER32	O9ER32 ratu...
9	1578	52.8	670	2 O9ER33	O9ER33 ratu...
10	1573.5	52.6	631	1 CNG3_MOUSE	O9J128 mus musculu
11	1568	52.5	663	1 CNG2_BOVIN	Q03041 bos taurus
12	1562.5	52.3	735	1 CNG1_CHICK	Q08005 gallus gall
13	1562	52.3	664	1 CNG2_BABIT	Q28718 oryctolagus
14	1558	52.1	664	1 CNG2_RAT	Q00195 ratu...
15	1558	52.1	664	2 O80XH6	O80XH6 mus musculu
16	1558	52.1	664	2 AAD41473	AAD41473 ratu...
17	1549.5	51.8	664	1 CNG3_HUMAN	Q16811 homo sapien
18	1547	51.8	664	1 CNG2_MOUSE	Q62398 mus musculu
19	1544.5	51.7	690	1 CNG1_BOVIN	Q00194 b cgm...
20	1544.5	51.7	698	2 O6ZNA7	O6ZNA7 homo sapien
21	1544.5	51.7	698	2 BADI8468	BADI8468 homo sapi
22	1538.5	51.5	686	1 CNG1_HUMAN	P29973 h cgm...
23	1538.5	51.5	686	2 Q9N0H4	Q9N0H4 sus scrofa
24	1533.5	51.3	684	1 CNG1_MOUSE	P29974 m cgm...
25	1532.5	51.3	693	1 CNG1_MOUSE	Q28279 c cgm...
26	1532	51.3	681	1 CNG1_RAT	Q62927 r cgm...
27	1529	51.2	645	1 CNG3_CHICK	Q09080 gallus gall
28	1519.5	50.8	637	2 O804I6	O804I6 carassius a
29	1436.5	48.1	682	1 CNG_ICPU	P55534 ictalunus p
30	1378.5	46.1	737	2 O8UVT8	O8UVT8 oncorhynch
31	1244.5	41.6	586	2 O7PW88	O7PW88 anopheles g

32	1235	41.3	665	1 CNG_DROME	Q24278 drosophila
33	1119.5	37.5	733	1 CNG_CAEEL	Q03611 caenorhabd
34	993	33.2	1218	2 O9W201	O9W201 drosophila
35	990.5	33.1	900	2 O97119	O97119 limulus pol
36	990	33.1	799	2 O7PTE6	O7PTE6 anopheles g
37	922	30.8	189	2 O6Q214	O6Q214 ratu...
38	922	30.8	189	2 AAS87325	AAS87325 ratu...
39	920	30.8	189	2 O6Q213	O6Q213 mus musculu
40	920	30.8	189	2 AAS87326	AAS87326 mus muscu
41	881.5	29.5	1126	2 O7Q9A9	O7Q9A9 anopheles g
42	879	29.4	1453	2 O8IR35	O8IR35 drosophila
43	879	29.4	1453	2 AAN09666	AAN09666 drosophila
44	879	29.4	1463	2 O9U5E2	O9U5E2 drosophila
45	879	29.4	1853	2 O9VXV8	O9VXV8 drosophila

ALIGNMENTS

RESULT 1
CNGX_RAT
ID CNGX_RAT
AC Q64359;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 29-MAR-2004 (Rel. 43, Last annotation update)
DE Cyclic-nucleotide-gated olfactory channel CNGC2 subunit.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=9437458; PubMed=7522325;
RA Bradley J., Li J., Davidson N., Lester H.A., Zinn K.;
RT "Heteromeric olfactory cyclic nucleotide-gated channels: a subunit
that confers increased sensitivity to cAMP."
RL Proc. Natl. Acad. Sci. U.S.A. 91:8890-8894(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Olfactory neuroepithelium;
RX MEDLINE=9500063; PubMed=7522482;
RA Liman E.R., Buck L.B.;
RT "A second subunit of the olfactory cyclic nucleotide-gated channel
confers high sensitivity to cAMP."
RL Neuron 13:611-621(1994).
RN [3]
RP SEQUENCE OF 7-35 FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Bradley J., Zhang Y., Bakin R., Lester H.A., Ronnett G., Zinn K.;
RT Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RL - FUNCTION: Odorant signal transduction is probably mediated by a G-
protein coupled cascade using cAMP as second messenger. The
olfactory channel can be shown to be activated by cyclic
nucleotides which leads to a depolarization of olfactory sensory
neurons.
CC - SUBUNIT: Heterooligomer of OCN1 and OCN2 subunits.
CC - SUBCELLULAR LOCATION: Integral membrane protein.
CC - TISSUE SPECIFICITY: Olfactory neurons.
CC - SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
(TC 1.A.1.5) family.
CC - SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC EMBL, U12623; AAA21464.1; -

541 MPEDMGZADDEAFEGSTGDSKDEGKAGQAPSGIE 575

Db

RESULT 2

ID 08177 PRELIMINARY; PRT; 474 AA.

AC 08177

DT 01-MAR-2003

DT 01-MAR-2003 (TRENDEL) 23 Created

DT 01-MAR-2004 (TRENDEL) 23 Last sequence update

CS Name-CHG44; (Fragment). 26, Last annotation update

OC Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi

OX Mammalia; Euteria; Primates; Catarrhini; Hominoidea; Homo.

RN NCBI TaxID=9606;

RP [1] _TaxID=9606;

RC SEQUENCE FROM N.A.

RA TISSUE=Brain;

RA MEDLINE=2288257; PubMed=1247792;

RA Strausberg R.L., Feingold E.S.;

RA Klausner R.D., Collins F.S.;

RA Altschul S.F., Zeeberg K.H., Sherman C.M.,

RA Hopkins R.P., Wainer L.H., Derge J.G.,

RA Stjepanko L., Marini J., Moore T., Schenck C.,

RA Brownstein L., Soares M.K., Farnes M.J., Bhat N.K.,

RA Rha S.S., Ueda T.B., Toeh M.F., Casavant T.L.,

RA Bock S.A., Miquelano N.A., Peters N.S., Hong L.,

RA Richards S., McManus P.J., Abelson R.D., Scherz T.E.,

RA Villalón D., Morley K.C., McKernan K.G., Johnson P.,

RA Paley J., Helk Muzny D.W., Hale S., Adams R.J.,

RA Whiting M., Madan E., Kettner J., Garcia A.M., J. Lu X.,

RA Blakesley R.W., Kettner J., Madan E., Rodriguez S.J.,

RA Rodriguez A.C., Touchman J.W., Green E.D., Bouffard G.G.,

RA Jona-Lasinio M.J., Skalska U., Schmitz U., Myers R.M.,

RT "Gene S.J., Maria Skalska U., Schmitz U., Myers R.M.,

RT and mouse CDNA and initial analysis of more than 15,000 full-length human

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]

RC SEQUENCE FROM N.A.

RA TISSUE=Brain;

RA Strausberg R.;

RA Submitter R.;

RA EMBL; R040277; ANH40277.1;

RA GO; GO:0016021; C:biological process;

RA GO; GO:0005267; F:ion channel activity; IEA.

RA GO; GO:0006813; P:ion transport; IEA.

RA InterPro; IPR000595; P:ion channel activity; IEA.

RA InterPro; IPR005821; C:ion binding; IEA.

RA Pfam; PF00027; C:ion channel; IEA.

RA Pfam; PF00027; C:ion channel; IEA.

RA SMART; SMART001; C:ion channel; IEA.

RA PROSITE; PS00888; C:ion channel; IEA.

RA PROSITE; PS00888; C:ion channel; IEA.

FT ION TRANSPORT; ION CHANNEL; TRANSMEMBRANE; TRANSPORT.

SO NON-TER

SEQUENCE 474 AA; 5433 MW; 269898587BBA01 CRC64;

Query Match

Best Local Similarity 100.0%; Score 2118; DB 2; Length 474;

Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps

21 RLRLVLDPSGDYYWMLNTWVFWYNNILIVCRACFPV

39 RKLPLVDDSGDYWYMLNTWVFWYNNILIVCRACFPV

0; Gaps

```

Db      158  LIDMVRFHTEGILVVDKGRISRYRTWSPFLDLASIMPTDVYVYRLGPHPTLR
Qy      200  LNRFLRPLREAPRTERTRTAYPNARFAXLMLEYFVYIHNMSCLYFALSRYLGGRDA
Db      218  LNRFLRPLREAPRTERTRTAYPNARFAXLMLEYFVYIHNMSCLYFALSRYLGGRDA
Qy      260  WYPPRPAQGFRLRRQYLYSFYFSTLITTTVGDTPPRAREEYLFMVGDFLAVMGFAT
Db      278  WYPPRPAQGFRLRRQYLYSFYFSTLITTTVGDTPPRAREEYLFMVGDFLAVMGFAT
Qy      320  IGMSSSVYNNMTADAFYPDHALVKKYMKLQHVNKLERVYIDWYQHLQINKKNTNEV
Db      338  IGMSSSVYNNMTADAFYPDHALVKKYMKLQHVNKLERVYIDWYQHLQINKKNTNEV
Qy      380  ALIQLPRLRAVAVSHLSTLSRVQIFONCEASLLEELVLTLOPQYSPGEYVCRKD
Db      398  ALIQLPRLRAVAVSHLSTLSRVQIFONCEASLLEELVLTLOPQYSPGEYVCRKD
Qy      423  IGOEWYIIRREGOLAVVADGGITQYAVLAGLYFGEISINIKG
Db      441  IGOEWYIIRREGOLAVVADGGITQYAVLAGLYFGEISINIKG

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RESULT 3

```

Q8JF90  PRELIMINARY; PRT; 609 AA.
ID      08JF90
AC      01-OCT-2002 (TREMBLrel. 22, Created)
DT      01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DE      01-MAR-2004 (TREMBLrel. 26, Last annotation update)
GN      Cyclic nucleotide-gated channel modulatory subunit CNCA4a.
OS      Ictalurus punctatus (Channel catfish).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC      Ictaluridae; Ictalurus.
OX      NCBI_TaxID=7998;
RN      [1]
RP      TISSUE=olfactory neuroepithelium;
RC      YAO H., Vosseshahi L.B., Tibbs G.R., Sun Z.-P., Young E.C.,
RA      Siegelbaum S.A.;
RL      Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR      GO:GO:0016021; C:integral to membrane; IEA.
DR      GO:GO:0005216; F:ion channel activity; IEA.
DR      GO:GO:0005267; F:potassium channel activity; IEA.
DR      GO:GO:0006813; P:ion transport; IEA.
DR      GO:GO:0006813; P:potassium ion transport; IEA.
DR      InterPro: IPR005095; CNMP binding.
DR      InterPro: IPR005821; Ion Trans.
DR      InterPro: IPR001622; K+channel_pore.
DR      Pfam: PF00027; CNMP_binding; 1.
DR      SMART: SM00100; CNMP; 1.
DR      PROSITE: PS00888; CNMP_BINDING_1; UNKNOWN_1.
DR      PROSITE: PS00889; CNMP_BINDING_2; 1.
DR      PROSITE: PS00892; CNMP_BINDING_3; 1.
KW      Ion transport; Ionic channel; Transmembrane; Transport.
SQ      SEQUENCE 609 AA; 70313 MW; 5C01AE4B3AB64D24 CRC64;

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Query Match 54.8%; Score 1638.5; DB 2; Length 609;

Best Local Similarity 55.5%; Pred. No. 2.2e-102; Indels 17; Gaps 4;

Matches 312; Conservative 94; Mismatches 139; Indels 17; Gaps 4;

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Qy      85  VLDPSGDYYWMLNTWVFPVYVNLILVGRACPPDLQHGVLVAVLVDYTSDDLVLVDV
Db      103  VLDPSSEFFYGMQVWVFPILYVWVILIRICFEVDQKQAVWYTLVDYISDLAVYADLF
Qy      145  VERHFGFLVGGILVVDKGRISRYRTWSPFLDLASIMPTDVYVYRLGPHPTLR
Db      163  IKVRTGYLBOGSLVRDMSRLKKRYLHSSQFLDVLVSQFLPTDLLVLSDFPKTPVVRINRFL

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Qy      205  RAPRLREAPRTERTRTAYPNARFAXLMLEYFVYIHNMSCLYFALSRYLGGRDAWYVD
Db      223  RSPRLSEALERNETATAYNIRISKMLILILHNMNCLYFALSRYLGSDDMWYVD
Qy      265  PRAQGFRLRRQYLYSFYFSTLITTTVGDTPPRAREEYLFMVGDFLAVMGFATMSGN
Db      283  TTDIEENSTRQYLYSFYFSTLITTTVGDTPPRAREEYLFMVGDFLAVMGFATMSGN
Qy      325  SSIVYNNMTADAFYPDHALVKKYMKLQHVNKLERVYIDWYQHLQINKKNTNEVALI
Db      343  GSIVNNKLRNDVFPNHELVSYSLSRRINRVAHWVYQHLQINKKNTNEVALI
Qy      385  LPERLRAVAVSHLSTLSRVQIFONCEASLLEELVLTLOPQYSPGEYVCRKDIGOEM
Db      403  LPTVLOTALVAVSHLSTLSRVQIFONCEASLLEELVLTLOPQYSPGEYVCRKDGHEM
Qy      445  YIIRREGOLAVVADGGITQYAVLAGLYFGEISINIKGMSGNRRYANIKSLGSLFCL
Db      463  YIIRREGOLAVVADGGITQYAVLAGLYFGEISINIKGMSGNRRYANIKSLGSLFCL
Qy      505  SKEDLREVSEYPOAQTIWEKGREILKMKLQVNAEAAEIALOATESRLRGDQOLD
Db      521  SKEDLREVSEYPOAQTIWEKGREILKMKLQVNAEAAEIALOATESRLRGDQOLD
Qy      555  DIQTKFARILAESSALKIAYRIERLEWQTEWMPEDL-----AEADDEGEPE----
Db      578  TIQTKLARLWVLESSVRGMGRVDELQTDGM---EGIVAGAGESEDDFERRRDVG
Qy      575  EGTSKDEGRASQGGPPPE
Db      600  DEGEQEEERPOEREGDGE

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RESULT 4

```

Q8JF90  PRELIMINARY; PRT; 551 AA.
ID      08JF90
AC      01-OCT-2002 (TREMBLrel. 22, Created)
DT      01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DE      01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE      Cyclic nucleotide-gated channel modulatory subunit CNCA4b truncated
DE      isoform.
GN      Name=CNCA4;
OS      Ictalurus punctatus (Channel catfish).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC      Ictaluridae; Ictalurus.
OX      NCBI_TaxID=7998;
RN      [1]
RP      TISSUE=olfactory neuroepithelium;
RC      YAO H., Vosseshahi L.B., Tibbs G.R., Sun Z.-P., Young E.C.,
RA      Siegelbaum S.A.;
RL      Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR      EMBL: AF522298; AAM70510.1; -.
DR      GO:GO:0016021; C:integral to membrane; IEA.
DR      GO:GO:0005216; F:ion channel activity; IEA.
DR      GO:GO:0005267; F:potassium channel activity; IEA.
DR      GO:GO:0006813; P:ion transport; IEA.
DR      GO:GO:0006813; P:potassium ion transport; IEA.
DR      InterPro: IPR005095; CNMP binding.
DR      InterPro: IPR005821; Ion Trans.
DR      InterPro: IPR001622; K+channel_pore.
DR      Pfam: PF00027; CNMP_binding; 1.
DR      Pfam: PF00520; Ion Trans.
DR      SMART: SM00100; CNMP; 1.
DR      PROSITE: PS00888; CNMP_BINDING_1; UNKNOWN_1.
DR      PROSITE: PS00889; CNMP_BINDING_2; 1.
DR      PROSITE: PS00892; CNMP_BINDING_3; 1.
KW      Ion transport; Ionic channel; Transmembrane; Transport.
SQ      SEQUENCE 551 AA; 63371 MW; 8C51F0B8854580D CRC64;

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Query Match 53.0%; Score 1585.5; DB 2; Length 551;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCB1_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97426406; PubMed=9278419;
 RA Miska T., Kusakabe Y., Emori Y., Gonoi T., Arai S., Abe K.;
 RT "Ratc buds have a cyclic nucleotide-activated channel, CNUGust.";
 RL J. Biol. Chem. 272:22623-22629(1997).
 DR EMBL; AB002801; BAA24353.1; -
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005216; F:ion channel activity; IEA.
 DR GO; GO:0005267; F:potassium channel activity; IEA.
 DR GO; GO:0006811; P:ion transport; IEA.
 DR GO; GO:0006813; P:potassium ion transport; IEA.
 DR InterPro; IPR000595; CNMP binding.
 DR InterPro; IPR005821; Ion trans.
 DR InterPro; IPR001622; K-channel pore.
 DR Pfam; PF00027; CNMP_binding; 1.
 DR Pfam; PF00520; Ion trans; 1.
 DR SMART; SMO0100; CNMP; 1.
 DR PROSITE; PS00888; CNMP_BINDING_1; 1.
 DR PROSITE; PS00889; CNMP_BINDING_2; 1.
 DR PROSITE; PS50042; CNMP_BINDING_3; 1.
 KW Ion transport; Ionic channel; Transmembrane; Transport.
 SQ SEQUENCE 611 AA; 70399 MW; 9ACECEP9EEF63AC4 CRC64;

Query Match 52.8%; Score 1578; DB 2; Length 611;
 Best Local Similarity 54.5%; Pred. No. 2.7e-98;
 Matches 300; Conservative 105; Mismatches 125; Indels 20; Gaps 5;

OY 14 PPAPSKARKLKP-VLDPSGDYVYVWMLNTVPPVWYNIILVGRACFPDLOHGYVAVMVL 72
 DB 68 PPEGCKGKKKPIVVDPSNNIYYRWLTAIPVFNWCLVCRACFDELQSHLTWLV 127
 OY 73 DYTSDLVILDMVYVYFHTGLEGILVYDKGRISRYRTWSFPLDASIMPTDVYVRL 132
 DB 128 DYSALALVYVMDLVARATGFLGQGLMVRDTRKLMGHYTKTLHPKLDIISLPTDLAVLKL 187
 OY 133 GPHPTLRLNPLRLAPRLFEAPDRTERTAAPNAPRIAKMLYIFVVIHNSCLYFALS 192
 DB 188 GMYPELRFNRLRLRSRLFEFPDRTERTNVNVFRIGNLVLYTLIIHMAACIFYALS 247
 OY 193 YLGFGRDAMVYVDPAPQGFEBRLROYLYSFYSTLILTTVGDTPPAREEYLFVWGDPL 252
 DB 248 FIGFTDSWVYVNPNSKPEYGRLSRKYISLYWSTLTLTIGETPPPVXDEEYLFVVIDFL 307
 OY 253 LAVMGFATIMSGSVIYNNMTADAAFYPDHALVKKYMKLOHVNKLEREYVIMYQHLQI 312
 DB 308 VGVILFATIVGVVSGMISNNASRAEFOAKLIDSIKQYQFVKVTKDLETRVIRWFDYVMA 367
 OY 313 NKMTNEVALIOLHPERLRAEVAVSVHLSTLSRVOIFONCEASLLEELVTLKLOPOTYSPG 372
 DB 368 NRKTVDEKVEVLKNLPDKLKAELAINVHLDLTKKRIIPDCCEAGLVELVTLKRAPVFSBG 427
 OY 373 EYVCRKGIQGEYMIYIRGQLAVVADGITYAVLAGLYGGEISIIINIKSGNSGRRTA 432
 DB 428 DYICKKGIDIGREMYIIRKGLAVVADGIVTQFVVLSDSYFGEISIIINIKSGNSGRRTA 487
 OY 433 NIKSLGYSDLFLCSKEDLREVLSEYPOAQTIEMEGREILIKMKNLD-----VNAEAELI 487
 DB 488 NIKSLGYSDLFLCSKEDLREVLSEYPOAQTIEMEGREILIKMKNLDIDDLVTARADANI 547
 OY 488 ALQATERSRLNGLDLQTKFARLLAELESSAKIAYIERLEWQ-TR-----EW 539
 DB 548 -----EKVEYLESSLDGLQTRFARLLAEYASQMKLQKRLSQLESQWTRRGHGFSPDR 601
 OY 540 EMPEDLAED 549
 DB 602 ENSEBASKAD 611

RESULT 8
 Q9ER32

ID Q9ER32 PRELIMINARY; PRT; 632 AA.
 AC Q9ER32;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DE Cyclic nucleotide-gated channel 2a.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCB1_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Olfactory epithelium, and Retina;
 RX MEDLINE=20442421; PubMed=10984544;
 RA Meyer M.R., Angele A., Kremmer B., Kaupp U.B., Mueller F.;
 RT "A cGMP-signalling pathway in a subset of olfactory sensory neurons.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:10595-10600(2000).
 DR EMBL; AJ272429; CAC09431.1; -
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005216; F:ion channel activity; IEA.
 DR GO; GO:0005267; F:potassium channel activity; IEA.
 DR GO; GO:0006811; P:ion transport; IEA.
 DR GO; GO:0006813; P:potassium ion transport; IEA.
 DR InterPro; IPR000595; CNMP binding.
 DR InterPro; IPR005821; Ion trans.
 DR InterPro; IPR001622; K-channel pore.
 DR Pfam; PF00027; CNMP_binding; 1.
 DR Pfam; PF00520; Ion trans; 1.
 DR SMART; SMO0100; CNMP; 1.
 DR PROSITE; PS00888; CNMP_BINDING_1; 1.
 DR PROSITE; PS00889; CNMP_BINDING_2; 1.
 DR PROSITE; PS50042; CNMP_BINDING_3; 1.
 KW Ion transport; Ionic channel; Transmembrane; Transport.
 SQ SEQUENCE 632 AA; 72535 MW; 2448AAECDD600D37 CRC64;

Query Match 52.8%; Score 1578; DB 2; Length 632;
 Best Local Similarity 54.5%; Pred. No. 2.9e-98;
 Matches 300; Conservative 105; Mismatches 125; Indels 20; Gaps 5;

OY 14 PPAPSKARKLKP-VLDPSGDYVYVWMLNTVPPVWYNIILVGRACFPDLOHGYVAVMVL 72
 DB 89 PPEGCKGKKKPIVVDPSNNIYYRWLTAIPVFNWCLVCRACFDELQSHLTWLV 148
 OY 73 DYTSDLVILDMVYVYFHTGLEGILVYDKGRISRYRTWSFPLDASIMPTDVYVRL 132
 DB 149 DYSALALVYVMDLVARATGFLGQGLMVRDTRKLMGHYTKTLHPKLDIISLPTDLAVLKL 208
 OY 133 GPHPTLRLNPLRLAPRLFEAPDRTERTAAPNAPRIAKMLYIFVVIHNSCLYFALS 192
 DB 209 GMYPELRFNRLRLRSRLFEFPDRTERTNVNVFRIGNLVLYTLIIHMAACIFYALS 268
 OY 193 YLGFGRDAMVYVDPAPQGFEBRLROYLYSFYSTLILTTVGDTPPAREEYLFVWGDPL 252
 DB 269 FIGFTDSWVYVNPNSKPEYGRLSRKYISLYWSTLTLTIGETPPPVXDEEYLFVVIDFL 328
 OY 253 LAVMGFATIMSGSVIYNNMTADAAFYPDHALVKKYMKLOHVNKLEREYVIMYQHLQI 312
 DB 329 VGVILFATIVGVVSGMISNNASRAEFOAKLIDSIKQYQFVKVTKDLETRVIRWFDYVMA 388
 OY 313 NKMTNEVALIOLHPERLRAEVAVSVHLSTLSRVOIFONCEASLLEELVTLKLOPOTYSPG 372
 DB 389 NRKTVDEKVEVLKNLPDKLKAELAINVHLDLTKKRIIPDCCEAGLVELVTLKRAPVFSBG 448
 OY 373 EYVCRKGIQGEYMIYIRGQLAVVADGITYAVLAGLYGGEISIIINIKSGNSGRRTA 432
 DB 449 DYICKKGIDIGREMYIIRKGLAVVADGIVTQFVVLSDSYFGEISIIINIKSGNSGRRTA 508
 OY 433 NIKSLGYSDLFLCSKEDLREVLSEYPOAQTIEMEGREILIKMKNLD-----VNAEAELI 487
 DB 509 NIKSLGYSDLFLCSKEDLREVLSEYPOAQTIEMEGREILIKMKNLDIDDLVTARADANI 568
 OY 488 ALQATERSRLNGLDLQTKFARLLAELESSAKIAYIERLEWQ-TR-----EW 539

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Db      569 -----EKEVYESSLDGLQTRFARLLAEVSASQMKLKORLSQLESQWTRRGHGFSPDR 622
Qy      540 EWPEDLEAD 549
Db      623 ENESEDASKAD 632

RESULT 9
Qy      09ER33      PRELIMINARY;      PRT;      670 AA.
ID      09ER33
AC      09ER33;
DT      01-MAR-2001 (TRENBLREL. 16, Created)
DT      01-MAR-2001 (TRENBLREL. 16, Last sequence update)
DT      01-MAR-2004 (TRENBLREL. 26, Last annotation update)
DE      Cyclic nucleotide-gated channel 2b.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxId=10116;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Olfactory epithelium;
MEDLINE=20442421; PubMed=10984544;
RA      Meyer M.R., Angele A., Kremmer E., Kaupp U.B., Mueller F.;
RT      "A cGMP-signalling pathway in a subset of olfactory sensory neurons.";
RL      Proc. Natl. Acad. Sci. U.S.A. 97:10595-10600(2000).
DR      EMBL, AJ272428; CAC09430.1; -.
DR      GO; GO:0016021; C:Integral to membrane; IEA.
DR      GO; GO:0005216; F:Ion channel activity; IEA.
DR      GO; GO:0005267; F:potassium channel activity; IEA.
DR      GO; GO:006811; P:ion transport; IEA.
DR      GO; GO:006813; P:potassium ion transport; IEA.
DR      InterPro; IPR000595; CNMP_binding.
DR      InterPro; IPR005821; Ion trans.
DR      InterPro; IPR001622; K+channel_pore.
DR      Pfam; PF00027; CNMP_binding. 1.
DR      Pfam; PF00520; ion trans. 1.
DR      SMART; SM00100; CNMP. 1.
DR      PROSITE; PS00888; CNMP_BINDING_1; 1.
DR      PROSITE; PS00889; CNMP_BINDING_2; 1.
DR      PROSITE; PS50042; CNMP_BINDING_3; 1.
DR      Ion transport; Ionic channel; Transmembrane; Transport.
SQ      SEQUENCE 670 AA; 76420 MW; 65203ADE6F85F62 CRC64;

Query Match      52.8%; Score 1578; DB 2; Length 670;
Beet Local Similarity 54.5%; Pred. No. 3.1e-98;
Matches 300; Conservative 105; Mismatches 125; Indels 20; Gaps 5;

Qy      14 PAPSPARKLTP-VLDPSGDYVYWMINTVFPVNYLILVGRACPPDLOHGLVAVLYL 72
Db      127 PPEGGKGRKDDPIVVDPSNIYRMLTALFVFNWCLLVGRACDELQSEHLTMTLV 186
Qy      73 DYTSDLLVLDVVRFRHTGLEQGLVVDKGRISRRVYRWTSFFLDLASEPTDVVYVL 132
Db      187 DYSADALVYVDMVLRARTEFLEQGLVAVRDTKLMKRYTTLHPKDIILSLIPDLAVLYL 246
Qy      133 GCHTFLPLRLARFLRABRLEAFARDRTETRAVYAPAFIAKLMIYFIVITWNSCLYALSR 192
Db      247 GMYVDELRLNRLRLRSRLREFPDRTETRNYPVRFIGNLVYTLIIHMNACIYPAISK 306
Qy      193 YLGFGRDAVYVDDPQGFERLROVLYSFYSTLILTVGDPPEPARREEVYLFVWGDTL 252
Db      307 FIFGFTDSVNVYNTSFEYGRISRKTIYLYWSTLTLLTIGTFPPVXDEEYLFVVIDL 366
Qy      253 LAVMGFATTGSMSSVYVYNNMTADAAFYPDHALVKKYMKLQHVNRRLERRVLDWYQHL 312
Db      367 VGVLLFATIVGVNVSWMNNSRAEFQAKIDISKQYMFRTKTKLLETRVIRWFDYLYA 426
Qy      313 NKKMTNEVAIIQHLPERLAELAVAVSHLSTLSVQFQNCSEASLEELVTLKQPOYVSG 372
Db      427 NKRIVDEKVKLNPDLKALAEIAINVAHLDLTKKVRIFQCEAGLVELVLRPAVFSFG 486
Qy      373 EYVCRKGDIGEMVYIIRREGQLVAVADGITYAVLGAAGLYFGELSIINIKGNMSGNRRTA 432

Db      487 DYICKGDIIGREMYIIEKGLAVVADGVTQFVVLSDGSYFGEISILINIKSGSKGNRRTA 546
Qy      433 NIKSLGYDLPCLSEDEREVLYSEYPOQTMEEGREILKMTLD-----VNAAAEI 487
Db      547 NIRSIGYDLPCLSDMETLTETYPDAKRLAEEGRQILMKNDIIDDLYTARADART 606
Qy      488 ALQEATESRLGLDQDLDLQTFARLLAELESSALKAIVRIERLEWQ-TR-----EW 539
Db      607 -----EKEVYESSLDGLQTRFARLLAEVSASQMKLKORLSQLESQWTRRGHGFSPDR 660
Qy      540 EWPEDLEAD 549
Db      661 ENESEDASKAD 670

RESULT 10
ID      CN33 MOUSE
AC      CN33 MOUSE      STANDARD;      PRT;      631 AA.
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      05-JUL-2004 (Rel. 44, Last annotation update)
DE      Cyclic-nucleotide-gated cation channel alpha 3 (CNG channel alpha 3)
DE      (CNG-3) (CNG3) (Cyclic nucleotide gated channel alpha 3) (Cone
DE      photoreceptor cGMP-gated channel alpha subunit).
GN      Name=Cnga3; Synonyms=Cng3;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxId=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6; TISSUE=Retina;
RX      MEDLINE=20273944; PubMed=10813773;
RX      DOI=10.1002/(SICI)1096-9861(20000522)421:1<80::AID-CNE5>3.0.CO;2-O;
RA      Hirano A.A., Hack I., Wessale H., Duvoisin R.M.;
RT      "Cloning and immunocytochemical localization of a cyclic nucleotide-
RT      gated channel alpha-subunit to all cone photoreceptors in the mouse
RT      retina.";
RL      J. Comp. Neurol. 421:80-94(2000).
RN      [2]
RP      SEQUENCE OF 95-631 FROM N.A.
RC      STRAIN=129/Sv;
RX      MEDLINE=99307448; PubMed=10377453;
RA      Biel M., Seeliger M., Pfeiffer A., Kohler K., Gerschner A., Ludwig A.,
RA      Jaisle G., Fausser S., Zrenner E., Hofmann F.;
RT      "Selective loss of cone function in mice lacking the cyclic
RT      nucleotide-gated channel CNG3.";
RL      Proc. Natl. Acad. Sci. U.S.A. 96:7553-7557(1999).
RN      [3]
RP      FUNCTION, AND SUBUNIT.
RX      MEDLINE=20130348; PubMed=10662822;
RA      Gerschner A., Zong X., Hofmann F., Biel M.;
RT      "Molecular cloning and functional characterization of a new modulatory
RT      cyclic nucleotide-gated channel subunit from mouse retina.";
RL      J. Neurosci. 20:1324-1332(2000).
RN      [1]
RP      FUNCTION: Visual signal transduction is mediated by a G-protein
coupled cascade using cGMP as second messenger. This protein can
be activated by cyclic GMP which leads to an opening of the cation
channel and thereby causing a depolarization of cone
photoreceptors. Essential for the generation of light-evoked
electrical responses in the rod-, green- and blue sensitive cones
(Bay similarity). Induced a flickering channel gating, weakened the
outward rectification in the presence of extracellular calcium,
increased sensitivity for h-cis diltiazem and enhanced the cAMP
efficacy of the channel when coexpressed with CNGB3.
CC      -1- SUBUNIT: Heterooligomeric complex with CNGB3.
CC      -1- TISSUE SPECIFICITY: Integral membrane protein.
CC      -1- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
(CC 1.A.1.5) family.
CC      -1- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.

```

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CC or send an email to license@isb-sib.ch.)
CC -----
DR EMBL; AJ243933; CAB89685.1; -.
DR EMBL; AJ238239; CAB42891.1; -.
DR EMBL; AJ238240; CAB42891.1; JOINED.
DR EMBL; AJ238241; CAB42891.1; JOINED.
DR MGJ; MGJ1341818; Cng3.3.
DR GO; GO:0005221; F:intracellular cyclic nucleotide activated c. . . ; IPI.
DR InterPro; IPR000595; Ion trans.
DR InterPro; IPR001622; K+channel_pore.
DR Pfam; PF00027; CNMP binding; 1.
DR PROSITE; PS00888; CNMP_BINDING_1; 1.
DR PROSITE; PS00889; CNMP_BINDING_2; 1.
DR PROSITE; PS50042; CNMP_BINDING_3; 1.
KW GMP-binding; Ion transport; Ionic channel; Multigene family;
KW Transmembrane; Vasion.
FT TRANSMEM 112 133 Potential.
FT TRANSMEM 244 264 Potential.
FT TRANSMEM 320 340 Potential.
FT NP_BIND 423 546 GCMF.
FT BINDING 490 490 GCMF.
FT BINDING 505 505 GCMF (Potential).
FT CONFLICT 110 110 GCMF (Potential).
FT CONFLICT 157 157 C -> Y (in Ref. 2).
FT CONFLICT 157 157 L -> V (in Ref. 2).
SQ SEQUENCE 631 AA; 72641 MW; 4FA8CD3B9A3FEECC CRC64;

Query Match 52.6%; Score 1573.5; DB 1; Length 631;
Best Local Similarity 54.4%; Pred. No. 5.8e-98;
Matches 296; Conservative 108; Mismatches 129; Indels 11; Gaps 3;

QY 2 SODIKVTTS-----PPAPKARKLP-VDPGSDYYVMWMLNVPVYNYLI 51
DB 67 SEIKVSTRSNQAPNPGEQKPPDGGEGRKEEIVVDESNICYCMILNALPYYNCL 126
QY 52 LVCRAGEPDLQHGVLVAMVLDVTSLLYLMLNMVVRPHTGLEGILVVDKRISSRYVR 111
DB 127 LVCRACFDELQSHLTLMLVLDVTSADVLLVLMVLRATGFLGQLAMRDTKRLMKHYTK 186
QY 112 TWSEFLDASLMPDVVYVRLGPHPTTLRLNFRAPLFEAPPTETRTYVNAFRIAK 171
DB 187 TLHFKLDLISLPTDLAYKLGVPYELRPNRLKFSLEFPDTRIRYVNVFRIGN 246
QY 172 LMLYLFVVIHNSCTYFALSRYLGRDPAVYPPDAQGFERLROYLYSEFSTLLIT 231
DB 247 LVLYTLIIHMACIYPAISKRTIGGDSWYPTSKREYARLSRKIYSGYVSTLLIT 306
QY 232 VDDTPPPAREBEYLFVWGDFLLAVWGFAITGSSSVIYMMNTADAFFYDHALYKYNK 291
DB 307 IGETPPPVKDEBYLFVVIDFLVGLITPATIGNGMSISMMNAPRVEFOAKIDSVQYQ 366
QY 292 LQHVNRKLERVIMYOHLOINKKMTNEVALLOHLPRLFAEVAVSVHLSTLSRVQIFON 351
DB 367 FRKYTKOLETRVIMFVYLMANRKTVEKEVLNKLDPKLAFAIAINVHLDLTKKRAIFOD 426
QY 352 CEASLLELVLYKOPQYTSFGEYVCRKGDIGEMVYIIRREGQLAVVADDDITQYAVLAGL 411
DB 427 CEAGLLELVLYKRPVTSFGEYVCRKGDIGEMVYIIRREGQLAVVADDDITQYAVLAGL 411
QY 412 YFGISITINIKGNMGRRTANIKSGYSLFCLSTEDLREVLSEYPOQITMEKREI 471
DB 487 YFGEISITINIKGSKGRRTANIKSGYSLFCLSTEDLREVLSEYPOQITMEKREI 471
QY 472 LLMKNLDVVAEAEALQEAATESRLGDDQDLDTQTFARLLAESSALKAIAIRER 531
DB 531 LLMKNLDVVAEAEALQEAATESRLGDDQDLDTQTFARLLAESSALKAIAIRER 531

DB 547 LMKCNLDIEDLVVARVDTRD-VREKYEYLESSLDLQTRFARLLAEYSQKKQKRLTR 605
QY 532 LEWQ 535
DB 606 LEWQ 609

RESULT 11
CNG2_BOVIN STANDARD; PRT; 663 AA.
AC 003041;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cyclic-nucleotide-gated olfactory channel (Cyclic-nucleotide-gated
DE cation channel 2) (CNG channel 2) (CNG-2) (CNG2).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Olfactory epithelium;
RX MEDLINE=91032022; PubMed=1699793;
RA Ludwig J., Margalit T., Bismann E., Lancet D., Kaup U.B.;
RT "Primary structure of cAMP-gated channel from bovine olfactory
RT epithelium."
RL FEBS Lett. 270:24-29(1990).
CC -1- FUNCTION: Odorant signal transduction is probably mediated by a G-
CC olfactory channel coupled cascade using cAMP as second messenger. The
CC nucleotides which leads to a depolarization of olfactory sensory
CC neurons.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Olfactory neurons.
CC -1- MISCELLANEOUS: The olfactory channel is activated by both cAMP and
CC GMP at similar concentrations, whereas the cAMP-gated channel is
CC much less sensitive to cAMP.
CC -1- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
CC (TC 1.A.1.5) family.
CC -1- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; X55010; CA38754.1; -.
DR PIR; S11521; S11521.
DR InterPro; IPR000595; CNMP binding.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR001622; K+channel_pore.
DR Pfam; PF00027; CNMP binding; 1.
DR PROSITE; PS00888; CNMP_BINDING_1; 1.
DR PROSITE; PS00889; CNMP_BINDING_2; 1.
DR PROSITE; PS50042; CNMP_BINDING_3; 1.
KW GMP-binding; Glycoprotein; Ion transport; Ionic channel;
KW Multigene family; Olfaction; Transmembrane.
FT TRANSMEM 1 140
FT TRANSMEM 141 160
FT TRANSMEM 161 173
FT TRANSMEM 174 192
FT TRANSMEM 193 216
FT TRANSMEM 217 236
FT TRANSMEM 237 274
FT TRANSMEM 275 297
FT TRANSMEM 298 349
DB 349
CYTOPLASMIC (Potential).
EXTRACELLULAR (Potential).
H2 (Potential).
H3 (Potential).
H4 (Potential).
CYTOPLASMIC (Potential).

```



```

Qy 303 VIDWYOHILQINKKTEVAILQHLPERLRAEVAVSHLSTLSRVOIFONCEASLJEELVLT 362
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 479 VIKWFDYIMTKKTVDEKEVYKKNLPDKKAIATNVHLDLTKKRIIODECAGLITELV 538
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 363 KLOPOTSPGPEYVKRDKDIGEMYYIIRREGOLAVVADGIGIYAVLGLYFGESITINIK 422
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 539 KUKRTVSPGPDYICKGKIGEMYYIIRREGOLAVVADGIGIYAVLGLYFGESITINIK 598
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 423 GNNSGNRRNTANIKSLGYSDLFCLSKEDLREVLSEYPOAOTIMEKREIILKNNKLDVNA 482
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 599 GSKSGNRRNTANIRISGYSDLFCLSKEDLREVLSEYPOAOTIMEKREIILKNNKLDVNA 658
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 483 EAAEIALQGEATSESLRELDOQDLQTKFARLAELESSALKIAYRIERLEWOTREMPMP 542
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 659 AKAG-ADPKLEEYIDRLTALDTLQTRFARLAEVSSSOQKVKORLARIVETRVKKY-G 716
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 543 EDLAEADDEGEPEEGTSKD 561
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 717 GSLSVGEPEPEKPEQK 735
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 13

CNG2_RABIT STANDARD; PRT; 664 AA.

```

ID CNG2_RABIT STANDARD; PRT; 664 AA.
AC Q28718;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cyclic-nucleotide-gated olfactory channel (Cyclic-nucleotide-gated
   cation channel 2) (CNG channel 2) (CNG2) (Aorta CNG channel)
DE (RACNG).
Name=CNGA2; Synonyms=CNGC2;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
   NCBI_Taxid=9986;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Aorta;
RX MEDLINE=93359035; PubMed=7689061;
RA Biel M., Altenhofen W., Hüllin R., Ludwig J., Freichel M.,
   "Primary structure and functional expression of a cyclic nucleotide-
   gated channel from rabbit aorta.";
RT FEBS Lett. 329:134-138(1993).
RL -1- FUNCTION: Odorant signal transduction is probably mediated by a G-
   protein coupled cascade using cAMP as second messenger. The
   olfactory channel can be shown to be activated by cyclic
   nucleotides which leads to a depolarization of olfactory sensory
   neurons.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
   (TC 1.A.1.5) family.
CC -1- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
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   modified and this statement is not removed. Usage by and for commercial
   entities requires a license agreement (See http://www.ebi.ac.uk/announcements
   or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; X59668; CAA42201.1; ALT INIT.
DR InterPro; IPR000595; cAMP binding.
DR InterPro; IPR005821; Ion Trans.
DR InterPro; IPR001622; K-channel_pore.
DR Pfam; PF00027; cAMP_binding; 1.
DR Pfam; PF00520; Ion_trans; 1.
DR PROSITE; PS00888; cAMP_BINDING_1; 1.
DR PROSITE; PS00889; cAMP_BINDING_2; 1.
DR PROSITE; PS50042; cAMP_BINDING_3; 1.
KW cAMP-binding; Ion transport; Ionic channel; Multigene family;

```

```

KM Olfaction; Transmembrane.
FT DOMAIN 1 140
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
FT TRANSMEM 141 160
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
FT TRANSMEM 161 173
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
FT TRANSMEM 174 192
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
FT TRANSMEM 193 216
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
FT TRANSMEM 217 236
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
FT TRANSMEM 237 274
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
FT TRANSMEM 275 297
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
FT TRANSMEM 298 349
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
FT TRANSMEM 350 369
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
FT TRANSMEM 370 453
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
FT TRANSMEM 454 474
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
FT NP_BIND 475 664
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
FT BINDING 462 584
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
FT BINDING 521 521
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
FT BINDING 536 536
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
FT CARBOHYD 379 379
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
SQ SEQUENCE 664 AA; 76205 MW; 5E9170DB322B3E9 CRC64;

```

Query Match 52.3%; Score 1562; DB 1; Length 664;
 Beet Local Similarity 54.2%; Pred. No. 3.7e-97;
 Matches 292; Conservative 108; Mismatches 133; Indels 6; Gaps 2;

```

Qy 18 SKARKLLPVLDPSGDYVYVWMLNTWVPVWYVNLIIYVGRACFPDLOHGYVAVMLVDTSD 77
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 124 TKKKFELFVLDPADMDYRMLFVYVAMPVLTNWCCLVARACPSDLOHGYVAVMLVDTSD 183
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 78 LLYLLDVAVRPHHTGEEQGLIVVDKGRISRYVRYTSFFFLDASLMPDTPVYVRLGPHTP 137
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 184 VVYIADFLFIRLRTGFEQGLVVDKGRISRYVRYTSFFFLDASLMPDTPVYVRLGPHTP 243
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 138 TLRNRLRARPRLFEAPDRTEETAYVNAFRIAKMLTYVTVYVHNSCLYFALSRYLGRG 197
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 244 ELRNRLRARPRLFEAPDRTEETAYVNAFRIAKMLTYVTVYVHNSCLYFALSRYLGRG 303
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 198 RDAMVYDPAQGFERLRYOYLSFFYSTLIITTVGDTPPAREEYLFVWVGDFLAWVG 257
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 304 VDTWVYVNTIDPEYGLAREYICLWSTLTLTITETPPVDEEYLVVIFDLGLVLI 363
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 258 PATTMGMSGVYVYVNTADAAFPDHALYKTYKLOHVRKLERRYIDWYOHILQINKKMT 317
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 364 FATVAVGVGSMISNNMNAFPAQKIDAYVHYVQFKEVKEAEKVIKWFVLTMTKTV 423
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 318 NEVAIIQHLPERLRAEVAVSHLSTLSRVOIFONCEASLJEELVLTQLOPOTSPGPEYVKR 377
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 424 DEBEVLAKNLPKARAIATNVHSLTKKRIIODECAGLITELVLTARPOVSPGDIYCR 483
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 378 KDIGEMYYIIRREGOLAVVADGIGIYAVLGLYFGESITINIKGNNSGNRRNTANIKSL 437
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 484 KDIGEMYYIIRREGOLAVVADGIGIYAVLGLYFGESITINIKGNNSGNRRNTANIRSL 543
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 438 GYSDLFCLSKEDLREVLSEYPOAOTIMEKREIILKNNKLDVNAEAA--EIALDEATES 495
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 544 GYSDLFCLSKEDLREVLSEYPOAOTIMEKREIILKNNKLDVNAEAA--EIALDEATES 599
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 496 RLRGLDQDLQTKFARLAELESSALKIAYRIERLEWOTREMPMPADDEADGEP 554
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 600 KIKOLETNETLTYTRFGRILAEYTAQKLRITVLEVRKQNTEDYDLSGNNSPP 658
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 14

CNG2_RAT STANDARD; PRT; 664 AA.

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ID CNG2_RAT STANDARD; PRT; 664 AA.
AC Q00195;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cyclic-nucleotide-gated olfactory channel (Cyclic-nucleotide-gated
   cation channel 2) (CNG channel 2) (CNG2) (OCNC1).
GN Name=Cnga2; Synonyms=Cngc2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```


DR EMBL; BC048775; AAH48775.1; -.
DR MGD; MGI:108040; Cnga2.
DR GO; GO:0005216; P:ion channel activity; IMP.
DR GO; GO:0007608; P:perception of smell; IMP.
DR InterPro; IPR000595; CNMP binding.
DR InterPro; IPR003938; EAG_ELK_ERG.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR001622; K+channel_pore.
DR Pfam; PF00027; CNMP binding; 1.
DR Pfam; PF00520; Ion trans; 1.
DR SMART; PR01463; EAGCHANL_FMLY.
DR PROSITE; PS00888; CNMP_BINDING_1; 1.
DR PROSITE; PS00889; CNMP_BINDING_2; 1.
DR PROSITE; PS00042; CNMP_BINDING_3; 1.
DR Ion transport; Ion channel; Transmembrane; Transport.
KW SEQUENCE 664 AA; 76192 MW; 34F8DF3B372C0D9C CRC64;
SQ

Query Match 52.1%; Score 1558; DB 2; Length 664;
Best Local Similarity 54.2%; Pred. No. 6,9e-97;
Matches 292; Conservative 107; Mismatches 134; Indels 6; Gaps 2;

QY 18 SKARLLVLDPSGDIYYWMTNTMVPVWYNLIIVCRACFPDLQHGIVAMLVLDYTS 77
Db 126 TKKKEFELVLDPAQDWMYRMLFVAMPVLYNCLVAPACFSDDLQNTYFVWLVLDYPSD 185

QY 78 LLYLDMVVRFRHTGFLQGIIVVDKGRISRYRTWSPFLDASIMPTDVVVRIGPHTP 137
Db 186 TVYINDLIIRLTGFLQGLVLDKPKLRDNYIHTLQFRLDVAIIPDILYFAVGISHP 245

QY 138 TLRLNRFAPRLFAFRTETRTAYPNAFRIAKMLYIFVVIHNSCLYFALSRYLQFG 197
Db 246 EVRFNRRLHFAMFEPFRTETRTSYPNIFRISNLVLYLVIHNNACIYVAISKISGFG 305

QY 198 RDAWVYPPDAQGFRLRQVLYSFYFTLLITVGDTPPAREREYLFMVGDFLLAMG 257
Db 306 VDTWYFNTDPEYGLAREYIYCYWSTLITLITGETPPVKDEEYLFVIPDFLIGVLI 365

QY 258 FATWGSMSVLYNNNTADAAFYPDHALVKKYMKLQHVNRKLERVIDMYCHLQINKKMT 317
Db 366 FATWGSMSVLYNNNTADAAFYPDHALVKKYMKLQHVNRKLERVIDMYCHLQINKKMT 425

QY 318 NEVALIQHLPERLRAEVAVSVHLSTLSRVQIFQNCESLLEELVLKLPQYSPGEYVCR 377
Db 426 DEREVLYKNLPKALRAEIAINVHLSTLKKVRIFQDCEAGLVELVLEKRPQVFPSPDYICR 485

QY 378 KADIGQEMYYIIRREGQLAVVADGDTQYAVLAGLYFGESIIINIKGNSGNRRRTANIKSL 437
Db 486 KGDICKEMYIIKEGKLAVVADGDTQYAVLAGLYFGESIIINIKGNSGNRRRTANIKSL 545

QY 438 GYSDFCLSKEDLREVLSEYFQAQTIMKEKREILLKNNKLDVNAEA-ETALQEATES 495
Db 546 GYSDFCLSKEDLREVLSEYFQAQTIMKEKREILLKNNKLDVNAEA-ETALQEATES 601

QY 496 RLRLGDDQDLQTFARLALAEBSALKIAYIRLERLWQTRWMPMPEDLAADDEGEP 554
Db 602 KLEQLETMTLTYRFARLAAYTGAQOKLQKRIIVLETKMKQNHEDDYLSDGINTPEP 660

Search completed: February 10, 2005, 03:42:45
Job time : 116 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 9, 2005, 23:11:20 ; Search time 27 Seconds
(without alignments)
2049.061 Million cell updates/sec

Title: US-09-927-267-1

Perfect score: 2989

Sequence: 1 MSQDTKVKTTESPPAPSKA.....EGTSKDEGRASQGPPE 575

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2811	94.0	575	2 I59327	olfactory cyclic n
2	1579	52.8	706	2 A55251	cyclic nucleotide-
3	1568	52.5	663	2 S11521	CAMP-gated channel
4	1562.5	52.3	735	2 I50630	alpha subunit of c
5	1562	52.3	732	2 S35691	cyclic nucleotide-
6	1558	52.1	664	2 S11517	cyclic nucleotide-
7	1544.5	51.7	690	1 S07103	CAMP-gated ion cha
8	1542	51.6	695	2 S74179	cyclic nucleotide-
9	1538.5	51.5	686	1 A44842	CAMP-gated ion cha
10	1532.5	51.3	691	2 JC6509	rod cyclic nucleot
11	1529	51.2	645	2 I50680	alpha subunit of r
12	1526.5	51.1	690	2 A42161	CAMP-gated cation
13	1525.5	51.0	688	2 B42161	CAMP-gated cation
14	1436.5	48.1	682	1 JH0560	cyclic nucleotide-
15	1235	41.3	665	2 S52072	DmCNC protein - f
16	1121.5	37.5	772	2 S28292	hypothetical prote
17	858	28.7	261	2 I78560	cyclic nucleotide-
18	847	28.3	261	2 I78559	cyclic nucleotide-
19	788.5	26.4	800	2 T19627	hypothetical prote
20	738	24.7	673	2 T20936	hypothetical prote
21	716	24.0	909	2 S32538	CAMP-gated cation
22	647	21.6	644	2 T33125	hypothetical prote
23	642	21.5	611	2 T20935	hypothetical prote
24	511.5	17.1	191	2 S74158	CAMP-gated cation
25	491.5	16.4	189	2 S74159	CAMP-gated cation
26	470.5	15.7	767	2 T21969	hypothetical prote
27	387.5	13.0	962	2 T53197	potassium channel
28	382.5	12.8	1087	2 T31100	probable potassium
29	382.5	12.8	1284	2 T13168	probable potassium

30	377.5	12.6	1174	2 A40853	potassium channel
31	377	12.6	989	2 I48912	potassium channel
32	375	12.5	1159	2 I38465	probable potassium
33	370	12.4	1102	2 T17367	potassium channel
34	365	12.2	934	2 T42394	potassium channel
35	362.5	12.1	514	2 T19579	hypothetical prote
36	362	12.1	1017	2 T33354	probable potassium
37	339.5	11.4	828	2 T52046	potassium channel
38	310.5	10.4	662	2 T04461	potassium channel
39	307.5	10.3	807	2 T12177	potassium channel
40	300	10.0	688	2 S55349	potassium channel
41	295.5	9.9	716	2 T51354	cyclic nucleotide-
42	293	9.8	787	2 S68699	potassium channel
43	285.5	9.6	845	2 T07052	probable potassium
44	269.5	9.0	887	2 T03939	potassium channel
45	268.5	9.0	838	2 S23606	potassium channel

ALIGNMENTS

RESULT 1

I59327
Olfactory cyclic nucleotide gated cation channel - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #ext_change 09-Jul-2004
C/Accession: I59327; I58165
R/Bradley, J.; Li, J.; Davidson, N.; Lester, H.A.; Zinn, K.
Proc. Natl. Acad. Sci. U.S.A. 91, 8890-8894, 1994
A/Title: Heteromeric olfactory cyclic nucleotide-gated channels: A new subunit that con

A/Reference number: I59327; M01D:94377458; PMID:7522325
A/Accession: I59327
A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA
A/Residues: 1-575 <RES>
A/References: UNIPROT:Q64359; EMBL:U12623; NID:G538128; PID:AAA21464.1; PID:G538

R/Liman, E.R.; Buck, L.B.
Neuron 13, 611-621, 1994
A/Title: A second subunit of the olfactory cyclic nucleotide-gated channel confers high

A/Reference number: I58165; M01D:95000663; PMID:7522482
A/Accession: I58165
A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA
A/Residues: 1-575 <RES>
A/References: EMBL:U12425; NID:G548083; PID:AAA64748.1; PID:G548084

C/Suprafamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>
F/348-472/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 94.0%; Score 2811; DB 2; Length 575;
Best Local Similarity 93.4%; Pred. No. 3e-187;
Matches 537; Conservative 16; Mismatches 22; Indels 0; Gaps 0;

QY	1	MSQDTKVKTTESPPAPSKALPVLDPSGDYYVMTWTFPPVMTLLIIVCRACFPD	60
DB	1	MSQDGKVKTTESPPAPSKAKLPLVDPSGDYYVMTWTFPPVMTLLIIVCRACFPD	60
QY	61	LQHGVLVAVLVLDYSDLLYLDMVRFHTGFLFEOGILLVVDKGRISRRVYRTWSFLDIA	120
DB	61	LQHSYLVAVFVLDYSDLLYLDMVRFHTGFLFEOGILLVVDKGRISRRVYRTWSFLDIA	120
QY	121	SLMPTDVVVRVLRGPHPTLRNLRFLAPRLFEAFDTERTRVAPNAFRLAKMLYIFVVI	180
DB	121	SLVPTDAVVOVLRGPHPTLRNLRFLAPRLFEAFDTERTRVAPNAFRLAKMLYIFVVI	180
QY	181	HNNSCLYFALSRYLGFGRDAMVYPPDAQGFELRRQYLYSPYFSTLILTTVGDTPPPAR	240
DB	181	HNNSCLYFALSRYLGFGRDAMVYPPDAQGFELRRQYLYSPYFSTLILTTVGDTPPPAR	240
QY	241	EEBYLFMVDDELAVVGFATINGSMSVYNNMTADAAPYPPDALVKKYMKLOHVNRKLE	300
DB	241	EEBYLFMVDDELAVVGFATINGSMSVYNNMTADAAPYPPDALVKKYMKLOHVNRKLE	300
QY	301	RRVIDWYOHLOINKKMTNEVALLOHLPERLRAEVAVSVHLSTLSRVOIFONCEASLLBEL	360

C:Superfamily: cyclic nucleotide-gated channel; CAMP receptor protein cyclic nucleotide-
C:Keywords: GMP binding
F:475-599/Domain: CAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 51.0%; Score 1525.5; DB 2; Length 688;
Best Local Similarity 51.9%; Pred. No. 66-98;
Matches 289; Conservative 116; Mismatches 137; Indels 15; Gaps 4;

QY 6 KKTTESSPAPSKARKLLPVLDPSGDYVYMWLNTMVPFVWNLIIIVGRACFPDIOHY 65
DB 133 KKKKEKTEKKEBEKEVEVVDISGNTYYNMFCTTLFVWNTMTIIRACFDELQSDY 192
QY 66 LVAMVLDTSDLLYLDMVVRFHGTGLEQGLIVVDKGRISRRYRTWSFFDLASLMT 125
DB 139 LEYMLIFDVSNVNVVLADMFVTRTCYGLQGLLVDMKMLIEKYKANLPKLDVLSVIT 252
QY 126 DVVYVRLGPHPTTLRLNRLPRLPRLPEAFDRTRTTPYNNARIKMLYIFVVIHWSG 185
DB 253 DLLYIKFGWNVYPEIRLRLRLRISRMEEFQRTETRTYNNIFRISNLVVIIVIIHWNAC 312
QY 186 LVEFALSRVILGFRDAMVYDPAQPGFERLRQYLSFVFEFTLLITVGDTPPPAREEYL 245
DB 313 VYYSISKALGFGNDTWVPDVPNDPFGRLARKYVSLVWSTLTTLTIGTPPEVLDSEY 372
QY 246 FVWGFLLAVMGFATIMSGMSSVIYNNMTADAFYPDHALVKKYMKLQHNKRLERRVD 305
DB 373 FVYVDFLIGVLFATIVGVSGISMNNAARAEFGORVAIKQYNNFRVNSDMERGVK 432
QY 306 WYQHLQINKMTNEVALLOHLPERLRAEYAVSVHLSLSRVOIPONCEASLLEEVYKIQ 365
DB 433 WFDYMTNKKTVDEDEEVRLNLPDLKRAEIAINVHDLTKKVRIFADCEAGLLVEVLKIQ 492
QY 366 POTVSGEVVCKGDIQGMYYIRREGQLAVVADDDGTQYAVGAGYRBEISINIKGM 425
DB 493 PÖVYVPGDITCKKGDIQGMYYIRREGQLAVVADDDGTQYAVGAGYRBEISINIKGM 552
QY 426 SGNRRNTANIKSLGYSDLPCLSKEDLEVLSEYPOAQTMEKGRREILLKMKLDVNA--- 481
DB 553 AGNRRNTANIKSLGYSDLPCLSKEDLEVLSEYPOAQTMEKGRREILLKMKLDVNA--- 612
QY 482 -AEAAEIALQEAETESRLGLDQQLDQITKPARLLAELESSALKIAYRIERLEWQTRMP 540
DB 613 GSDPMDL-----EEKYVTMEGSDVLDLQTRFACILAEYSMOOKLQKRLTKVEKFK--P 664
QY 541 WEEDLADEADDE--GEPE 555
DB 665 LIETEFSAIEEPGSE 681

RESULT 14

JH0560
Cyclic nucleotide-gated channel - channel catfish
C:Species: Ictalurus punctatus (channel catfish)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #ext_change 09-Jul-2004
C:Accession: JH0560
R:Goulding, E.H.; Ngai, J.; Kramer, R.H.; Colicos, S.; Axel, R.; Siegelbaum, S.A.; Chase
Neuron 8, 45-58, 1992
A:Title: Molecular cloning and single-channel properties of the cyclic nucleotide-gated
A:Reference number: JH0560; MUID:92110008; PMID:1370374
A:Accession: JH0560
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-682 <CGU>
A:Cross-references: UNIPROT:P55934; GB:M83111
A:Experimental source: olfactory epithelium
C:Comment: This cyclic nucleotide-gated channel is activated equally well by both CAMP &
C:Superfamily: cyclic nucleotide-gated channel; CAMP receptor protein cyclic nucleotide-
C:Keywords: CAMP binding; GMP binding; ion channel; ion transport; olfaction; transmem-
F:137-157/Domain: transmembrane #status predicted <TS1>
F:173-193/Domain: transmembrane #status predicted <TS2>
F:217-236/Domain: transmembrane #status predicted <TS3>
F:241-261/Domain: transmembrane #status predicted <TS4>
F:277-297/Domain: transmembrane #status predicted <TS5>

F:319-337/Domain: transmembrane #status predicted <TS5>
F:350-370/Domain: transmembrane #status predicted <TS6>
F:447-571/Domain: CAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 48.1%; Score 1436.5; DB 1; Length 682;
Best Local Similarity 49.8%; Pred. No. 8-9e-92;
Matches 288; Conservative 100; Mismatches 165; Indels 25; Gaps 6;

QY 11 ESSPAPSKARKLLP-----VLDPSGDYVYMWLNTMVPFVWNLIIIVGRACFPDIOHY 65
DB 110 QSAAPADAPKCTFKERWEGFVVSQSDDIYYVLFALASLWNMTILVGRACFDQQLDEN 169
QY 66 LVAMVLDTSDLLYLDMVVRFHGTGLEQGLIVVDKGRISRRYRTWSFFDLASLMT 125
DB 170 FFLWGLDGLGVYIYLDTCIRLRTGYLEQGLLVDMKMLIEKYKANLPKLDVLSVIT 229
QY 126 DVVYVRLGPHPTTLRLNRLPRLPRLPEAFDRTRTTPYNNARIKMLYIFVVIHWSG 185
DB 230 ELLFPVGTG--YVQLFRNRLRFSRMEEFDRTRTTPYNNARIKMLYIFVVIHWSG 288
QY 186 LVEFALSRVILGFRDAMVYDPAQPGFERLRQYLSFVFEFTLLITVGDTPPPAREEYL 245
DB 289 IYVYISKALGSLDVTWVYSGQN---KTLSPCYVCFWSTLTTLTIGMPPEVLDSEY 344
QY 246 FVWGFLLAVMGFATIMSGMSSVIYNNMTADAFYPDHALVKKYMKLQHNKRLERRVD 305
DB 345 FVYVDFLIGVLFATIVGVSGISMNNAARAEFGORVAIKQYNNFRVNSDMERGVK 404
QY 306 WYQHLQINKMTNEVALLOHLPERLRAEYAVSVHLSLSRVOIPONCEASLLEEVYKIQ 365
DB 405 WFDYMTNKKTVDEDEEVRLNLPDLKRAEIAINVHDLTKKVRIFADCEAGLLVEVLKIQ 464
QY 366 POTVSGEVVCKGDIQGMYYIRREGQLAVVADDDGTQYAVGAGYRBEISINIKGM 425
DB 465 PÖVYVPGDITCKKGDIQGMYYIRREGQLAVVADDDGTQYAVGAGYRBEISINIKGM 524
QY 426 SGNRRNTANIKSLGYSDLPCLSKEDLEVLSEYPOAQTMEKGRREILLKMKLDVNAEA 485
DB 525 MGNRRNTANIKSLGYSDLPCLSKEDLEVLSEYPOAQTMEKGRREILLKMKLDVNAEA 584
QY 486 EIALQEAETESRLGLDQQLDQITKPARLLAELESSALKIAYRIERLEWQTRMP 542
DB 585 GLGVLD--TEEKYERLDASLDIILQTRFARLLGFTSTQRLKORITALERQLCHTGLIS 643
QY 543 EDLAE-----ADDEGEPEEGTSKDEGRASQE 569
DB 644 DNEAGEHAGVPTHTHADIHAQPTHRTTSSETNSEE 681

RESULT 15

S52072
DmCNGC protein - fruit fly (Drosophila sp.)
C:Species: Drosophila sp.
C:Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #ext_change 16-Jul-1999
C:Accession: S52072
R:Baumann, A.; Frings, S.; Godde, M.; Seifert, R.; Kaupp, U.B.
EMBO J, 13, 5040-5050, 1994
A:Title: Primary structure and functional expression of a Drosophila cyclic nucleotide-
A:Reference number: S52072; MUID:95045396; PMID:7957070
A:Accession: S52072
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-665 <BAU>
C:Genetics:
A:Gene: FlyBase:Cng
A:Cross-references: FlyBase:FBgn0014462
C:Superfamily: cyclic nucleotide-gated channel; CAMP receptor protein cyclic nucleotide-
F:429-553/Domain: CAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 41.3%; Score 1235; DB 2; Length 665;
Best Local Similarity 47.1%; Pred. No. 8-3e-78;
Matches 243; Conservative 98; Mismatches 165; Indels 10; Gaps 2;

